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# SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB# 61227

Requester's Full Name: John Yin Examiner #: 69507 Date: 5-22-02  
 Art Unit: 1646 Phone Number 308-4008 Serial Number: 09/731657  
 Mail Box and Bldg/Room Location: 10B1501 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*  
 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

*Please search SEQ ID NO: 2 of 09/731657.*

## STAFF USE ONLY

Contact: Alexandra Wacławiw  
 Technical Info. Specialist  
 QM1 6A02 Tel: 308-4491

Searcher Phone: \_\_\_\_\_

Searcher Location: \_\_\_\_\_

Date Searcher Picked Up: 5-23-02

Date Completed: 5-23-02

Searcher Prep & Review Time: 05

Clerical Prep Time: \_\_\_\_\_

Online Time: 8

## Type of Search

NA Sequence (#) \_\_\_\_\_

AA Sequence (#) 1

Structure (#) \_\_\_\_\_

Bibliographic \_\_\_\_\_

Litigation \_\_\_\_\_

Fulltext \_\_\_\_\_

Patent Family \_\_\_\_\_

Other \_\_\_\_\_

## Vendors and cost where applicable

STN 1

Dialog \_\_\_\_\_

Questel/Orbit \_\_\_\_\_

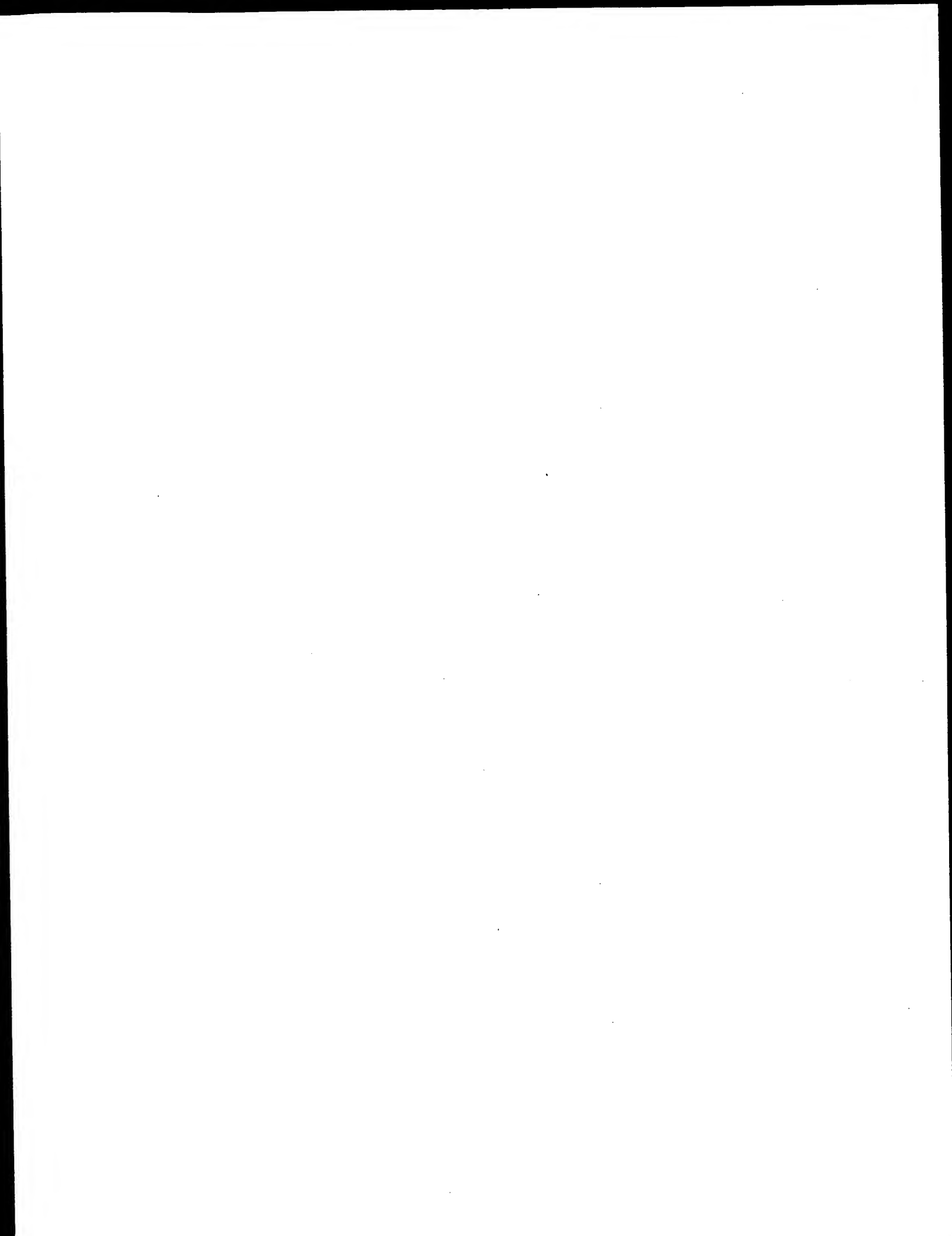
Dr. Link \_\_\_\_\_

Lexis/Nexis \_\_\_\_\_

Sequence Systems \_\_\_\_\_

WWW/Internet \_\_\_\_\_

Other (specify) Compuizer



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 23, 2002, 07:35:15 ; Search time 39.07 Seconds  
(without alignments)  
2950.975 Million cell updates/sec

Title: US-09-731-657-2

Perfect score: 5352

Sequence: 1 SQPEDASGRCAQRFSTLFSE.....GRMALRRTSKRGLHFIEQM 1038

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_032802.\*

Query	Match	Length	ID	Description
1:	100.0	1038	18	AAW35903
2:	97.5	1013	21	AAW01247
3:	32.5	328	22	AAW24057
4:	27.0	1220	22	AAW00195
5:	1446	27.0	1221	AAW00191
6:	1446	27.0	1221	AAW00199
7:	1446	27.0	1221	AAW00194
8:	1446	27.0	1250	AAW00190
9:	1446	27.0	1250	AAW00198
10:	1444.5	27.0	1192	AAW00712
11:	1444.5	27.0	1192	AAW00719
12:	1444.5	27.0	1192	AAW00712
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14:	1444.5	27.0	1192	AAW00712
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19:	1444.5	27.0	1192	AAW00712
20:	1444.5	27.0	1192	AAW00712
21:	1444.5	27.0	1192	AAW00712
22:	1444.5	27.0	1192	AAW00712

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	1446	27.0	1221	22	AAW00191
6	1446	27.0	1221	22	AAW00199
7	1446	27.0	1221	22	AAW00194
8	1446	27.0	1250	22	AAW00190
9	1446	27.0	1250	22	AAW00198
10	1444.5	27.0	1192	22	AAW00712
11	1444.5	27.0	1192	22	AAW00719

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13	1444.5	27.0	1193	22	AAU00716	Human novel G-prot
14	1444.5	27.0	1221	22	AAU00210	Human novel G-prot
15	1444.5	27.0	1222	22	AAU00206	Human novel G-prot
16	1444.5	27.0	1222	22	AAU00715	Human novel G-prot
17	1372.5	25.6	512	22	AAU00203	Human novel G-prot
18	1372.5	25.6	512	22	AAU00203	Human novel G-prot
19	1372.5	25.6	512	22	AAU00203	Human novel G-prot
20	1205	22.5	1111	22	AAU00202	Human novel G-prot
21	1205	22.5	1111	22	AAU00202	Human novel G-prot
22	1205	22.5	1112	22	AAU00193	Human novel G-prot
23	1203.5	22.5	1083	22	AAU00201	Human novel G-prot
24	1203.5	22.5	1084	22	AAU00714	Human novel G-prot
25	1203.5	22.5	1084	22	AAU00209	Human novel G-prot
26	1131.5	21.1	403	22	AAU00718	Human novel G-prot
27	651.5	12.2	687	21	AAU00205	Human novel G-prot
28	630	11.8	687	21	AAU00205	Human novel G-prot
29	629	11.8	687	21	AAU00205	Human novel G-prot
30	625	11.7	687	21	AAU00205	Human novel G-prot
31	624	11.7	512	22	AAU00205	Human novel G-prot
32	624	11.7	512	22	AAU00205	Human novel G-prot
33	617.5	11.5	693	20	AAU00238	Human novel G-prot
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42	604	11.3	549	21	AAU00238	Human novel G-prot
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57	533	10.0	872	21	AAU00238	Human novel G-prot
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66	523.5	9.8	1240	21	AAU00238	Human novel G-prot
67	523	9.8	1240	21	AAU00238	Human novel G-prot
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77	503.5	9.4	1469	20	AAU00238	Human novel G-prot
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79	502.5	9.4	1474	21	AAU00238	Human novel G-prot
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85 501.5 9.4 661 22 AAU18138 Novel human uterin  
86 501.5 9.4 661 22 AAU18399 Human endocrine po  
87 501.5 9.4 661 22 AAU16983 Human novel secret  
88 500.5 9.4 652 21 AAY59300 Human EGPCR polype  
89 497 9.3 453 21 AAY94340 Human cell surface  
90 495 9.2 190 22 AAM93518 Human polypeptide,  
91 494 9.2 2405 21 AAB21292 Human OREX ORF1956  
92 494 9.2 2560 22 ABB11404 Human FLAMINGO 1 h  
93 494 9.2 2923 22 AAU07054 Human Flamingo pol  
94 494 9.2 2956 22 AAU07053 T-cell surface ant  
95 491.5 9.2 835 19 AAM48756 Human CD97 protein  
96 491.5 9.2 835 20 AAY41090 Human CD97 protein  
97 491.5 9.2 835 21 AAB15728 Human novel G-prot  
98 487 9.1 359 22 AAE04451 Human novel G-prot  
99 486.5 9.1 217 22 AAG16226 Novel human diagno  
100 481.5 9.0 831 21 AAB01248 Human CD97 recepto

ALIGNMENTS

RESULT 1  
AAW36903  
ID AAW36903 standard; Protein: 1038 AA.

XX AC AAW36903;

XX DT 11-MAY-1998 (first entry)

XX DE Human epididymis-specific receptor protein.

XX KW Epididymis-specific receptor protein; transmembrane protein;  
XX KW sperm maturation; male infertility; agonist; antagonist;  
XX KW contraception; autoantibody; diagnostic; detection; human.

XX OS Homo sapiens.

XX FH Key . Location/Qualifiers  
XX FT Protein 1..1038  
XX FT /note="partial protein sequence"

XX FN DE19617940-A1.

XX PD 30-OCT-1997.

XX PF 29-APR-1996; 96DE-1017940.

XX PR 29-APR-1996; 96DE-1017940.

XX PA (IHFH-) IHF INST HORMON & FORTPFLANZUNGS.

XX PA (HORM-) INST HORMON & FORTPFLANZUNGSFORSCHUNG GM.

XX PI Ivell R, Osterhoff C;

XX WPI; 1997-527841/49.

XX DR N-PSDB; AAT97955.

XX PT DNA encoding epididymis-specific receptor protein - useful for

XX PT developing male infertility or contraceptive treatments

XX PS Claim 1; Page 19-22; 33pp; German.

XX CC This sequence represents a novel epididymis-specific receptor protein  
XX CC which is a transmembrane protein associated with the epididymis  
XX CC epithelium and is closely connected with sperm maturation. The protein  
XX CC or its derivative or fragments may be useful for detecting autoantibodies  
XX CC in the serum of infertile men and for developing ligands specific for the  
XX CC receptor, e.g. agonists that may stimulate sperm maturation and thus be  
XX CC useful for treating male infertility or antagonists that may be useful  
XX CC for contraception. The antibodies can be used to detect the receptor in  
XX CC vitro or in vivo. Oligonucleotides derived from the DNA sequences can  
XX CC be used as diagnostic probes.

SQ Sequence 1038 AA;  
Query Match 100.0%; Score 5352; DB 18; Length 1038;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SQPDASGRCAORFSTLSELAVRMVFSVRCQGHVGRTERVLLTFKIFLVLCIHLVVLVT 60  
DB 1 sqpedasgrcagrfscliselavrmvsvrqcghvgrteevlltfkiflvcihlvvlvt 60  
QY 61 SLEEDTNSLSLPPAKLVSVFAPSNEVETLSLNDVTLSSLPSNETEKTKITIVTTFN 120  
DB 61 sleedtdnsslsppekalsvsvfapsnevettlsldvttlsllpsnetektkitivtkfn 120  
QY 121 ASGVKPPORNICNLSSITCNDASAFRGETIMFYQDKESTVPQNOHITNGTLTGVLSELKRS 180  
DB 121 asgvkppornicnlsslscndsafrgelmfqdkestvppqnhlcnngltgvlselkrs 180  
QY 181 ELNKTLOTSETYFIMCATAEAQSTLNCTFTIKLNTMTNACAATAALERVKIRPMEHCCC 240  
DB 181 elnktlotsetyfimcataeaqstlnctftiklntmtnacaataalervkirmehccc 240  
QY 241 SVRIPCSPSEELGKLCQDLQDPVCLADHPGPPFPSSSSQSIPIVPRATVLSQVPKATSF 300  
DB 241 svripccspseelgklqcdlqdpivcladhprgppfssssqsiipivpratvlsqvpkatsf 300  
QY 301 AEPDYSPTVHNVPSPIGEIQPLSPOPSAPIASSPAIDMPPQSETISSPMPQTHVSGTTP 360  
DB 301 aepdydysptvhnvpvspigeqplspospsapiasspaiddmppssetisspmpqthvsgtpp 360  
QY 361 PVKAFSSPTVSAPANVTTSAPPVQTDIVNTSISDLENOVLQMERKALSLSLEPNLAG 420  
DB 361 pvkasfssptvsapanvtttsappvqtdivntssisdlenovlqmerkalslslepnlag 420  
QY 421 EMINQVSRLLHSPDMLAPLAQRLLKVVDDIGLQNLNNTISTSPSLALAVIRVNASS 480  
DB 421 eminqvsrllhspddmlaplaqrllkvddigqlnfnsttisltspslalatavirvnass 480  
QY 481 FNTTFVAQDPANLQVSLETQAPENSIGTITLPSLMMNLPAHDMELASRVQNFETPA 540  
DB 481 fnttfvaqdpnanlqvsletqapensigtitlpslmmnlpahdmelasrvqnfetpa 540  
QY 541 LFQDPSLENLSLISYVISSVANLTVRNLTNRVTTLKHINPSQDELTVRCVFWDLGRNG 600  
DB 541 lfqdpklenlslyviassvanltvrnltnrvttlkhinpsqdeltvrcvfwdlgrng 600  
QY 601 GRGGWSDNGCSVKDRRLNETICTCSHLTSFGVLQDLQSLVLPQAQMMALTFTYICCGLS 660  
DB 601 grggwsgdngcsvkdrlnetictcshltsfgvllqdlqslvlpqaqmmaltftyiccgls 660  
QY 661 SIFLSVTLVTYIAFEKIRRDYPSKILQALCAALLLNLFLLDSWIALYKMGGLCISAV 720  
DB 661 siflsvtlvtlyiafekirrdypsakilqalcaalllnlflldswialykmggglcisav 720  
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DB 721 flhyflvstwmgleafhmylalkvfntryirkylkfcivgngvpavvvtiltispsd 780  
QY 781 NYGLGSYGFPPNGSPDDFCWINNNAVFYITVVGVCVIFLLNVMFIVVVLVOLCRKIKKK 840  
DB 781 nyglgsygykfpngspddfcwinnnavfyitvvgvcvifllnvmfivvvlvolcrikkkk 840  
QY 841 QLGAQRKTSIQDLRSIAAGLTFLLGITWGFAPFANGPVNVTMYLFAFNTLOGFFTFIF 900  
DB 841 qlgaqrktsiqdlrsiaagltfllgitwgfapfngvpvntmylfaifntlogfftfify 900  
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QY 961 STTLVNVNDCSVHASGNGNASTERNVGSFVQNGDVCLHDTFGKHMFNEKEDSCMGKR 1020  
DB 961 sttlvvnvndcsvhasgngnasternvgsfvqngdvclhdtfgkhmfnekedscmgkr 1020

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 23, 2002, 07:35:20 ; Search time 17.89 seconds  
(without alignments)  
1417.203 Million cell updates/sec

Title: US-09-731-657-2

Perfect score: 5352

Sequence: 1 SQPDASGRCAQRFSTLTFSE.....GRMALRRTSKRGLHFIEQM 1038

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*

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6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501.5	9.4	521	4	US-08-956-322-4
2	501.5	9.4	652	4	US-08-956-322-2
3	500.5	9.4	652	3	US-09-110-116-1
4	463	8.7	344	3	US-09-110-116-4
5	438	8.2	886	3	US-09-110-116-3
6	411.5	7.7	1052	2	US-08-852-806-2
7	411.5	7.7	1052	3	US-09-163-669-2
8	367.5	6.9	884	2	US-08-465-976A-2
9	367.5	6.9	884	2	US-08-982-412-2
10	290	5.4	240	4	US-09-370-098-5
11	286	5.3	235	4	US-09-370-098-6
12	245.5	4.6	231	4	US-09-370-098-4
13	240.5	4.5	1324	2	US-08-811-897A-56
14	233	4.4	448	2	US-08-811-897A-18
15	233	4.4	448	2	US-08-855-213-18
16	233	4.4	467	2	US-08-811-897A-19
17	233	4.4	467	2	US-08-855-213-19
18	231.5	4.3	448	2	US-08-811-897A-16
19	231.5	4.3	448	2	US-08-855-213-16
20	231.5	4.3	485	2	US-08-811-897A-17
21	231.5	4.3	485	2	US-08-855-213-17
22	231	4.3	476	2	US-08-811-897A-20
23	231	4.3	476	2	US-08-855-213-20
24	231	4.3	495	2	US-08-811-897A-21
25	231	4.3	495	2	US-08-855-213-21
26	230	4.3	415	1	US-08-110-286A-6
27	230	4.3	415	4	US-08-981-189B-10

28	228.5	4.3	476	2	US-08-811-897A-14	Sequence 14, Appl
29	228.5	4.3	476	2	US-08-855-213-14	Sequence 14, Appl
30	228.5	4.3	513	2	US-08-811-897A-15	Sequence 15, Appl
31	228.5	4.3	513	2	US-08-855-213-15	Sequence 15, Appl
32	227.5	4.3	448	2	US-08-811-897A-22	Sequence 22, Appl
33	227.5	4.3	448	2	US-08-855-213-22	Sequence 22, Appl
34	227.5	4.3	525	2	US-08-811-897A-23	Sequence 23, Appl
35	227.5	4.3	525	2	US-08-855-213-23	Sequence 23, Appl
36	226.5	4.2	376	2	US-08-465-976A-3	Sequence 3, Appl
37	226.5	4.2	376	2	US-08-982-412-3	Sequence 3, Appl
38	226	4.2	415	1	US-08-110-286A-2	Sequence 2, Appl
39	225	4.2	475	2	US-08-811-897A-26	Sequence 26, Appl
40	225	4.2	475	2	US-08-855-213-26	Sequence 26, Appl
41	225	4.2	552	2	US-08-811-897A-27	Sequence 27, Appl
42	225	4.2	552	2	US-08-855-213-27	Sequence 27, Appl
43	224.5	4.2	476	2	US-08-811-897A-24	Sequence 24, Appl
44	224.5	4.2	476	2	US-08-855-213-24	Sequence 24, Appl
45	224.5	4.2	553	2	US-08-811-897A-25	Sequence 25, Appl
46	224.5	4.2	553	2	US-08-855-213-25	Sequence 25, Appl
47	215.5	4.0	431	4	US-08-981-189B-13	Sequence 13, Appl
48	214.5	4.0	431	1	US-08-381-433A-2	Sequence 2, Appl
49	214.5	4.0	476	2	US-08-811-897A-28	Sequence 28, Appl
50	214.5	4.0	476	2	US-08-855-213-28	Sequence 28, Appl
51	214.5	4.0	553	2	US-08-811-897A-29	Sequence 29, Appl
52	214.5	4.0	553	2	US-08-855-213-29	Sequence 29, Appl
53	209	3.9	411	1	US-08-381-433A-4	Sequence 4, Appl
54	209	3.9	411	4	US-08-981-189B-12	Sequence 12, Appl
55	208	3.9	431	4	US-08-981-189B-11	Sequence 11, Appl
56	205	3.8	449	1	US-08-142-439A-5	Sequence 5, Appl
57	205	3.8	449	2	US-08-869-477-5	Sequence 5, Appl
58	199.5	3.7	463	1	US-08-142-439A-2	Sequence 2, Appl
59	199.5	3.7	463	2	US-08-869-477-2	Sequence 2, Appl
60	197	3.7	411	1	US-08-381-433A-8	Sequence 8, Appl
61	188.5	3.5	437	2	US-08-538-816A-2	Sequence 2, Appl
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63	188.5	3.5	437	4	US-09-208-396-2	Sequence 2, Appl
64	187.5	3.5	462	3	US-09-238-796-2	Sequence 2, Appl
65	185.5	3.5	472	5	PCT-US94-09235-2	Sequence 2, Appl
66	185	3.5	515	2	US-08-468-249A-18	Sequence 18, Appl
67	185	3.5	585	1	US-08-142-439A-6	Sequence 6, Appl
68	185	3.5	585	2	US-08-142-551B-125	Sequence 125, Appl
69	185	3.5	585	2	US-08-869-477-6	Sequence 6, Appl
70	185	3.5	585	2	US-08-468-249A-19	Sequence 19, Appl
71	183	3.4	593	2	US-08-468-249A-21	Sequence 21, Appl
72	181	3.4	591	2	US-08-468-249A-20	Sequence 20, Appl
73	180	3.4	485	1	US-08-453-956-15	Sequence 15, Appl
74	180	3.4	485	1	US-08-086-631-15	Sequence 15, Appl
75	180	3.4	485	2	US-08-452-930-15	Sequence 15, Appl
76	180	3.4	485	5	PCT-US93-08174-15	Sequence 15, Appl
77	179	3.3	458	1	US-08-112-817C-2	Sequence 2, Appl
78	177.5	3.3	477	1	US-08-453-742-27	Sequence 27, Appl
79	177.5	3.3	477	1	US-08-454-464-27	Sequence 27, Appl
80	177.5	3.3	477	1	US-08-453-222-27	Sequence 27, Appl
81	177.5	3.3	477	1	US-08-452-802-27	Sequence 27, Appl
82	177.5	3.3	541	3	US-08-468-011A-2	Sequence 2, Appl
83	177.5	3.3	541	4	US-09-236-468A-2	Sequence 2, Appl
84	177.5	3.3	541	5	PCT-US95-07085-2	Sequence 2, Appl
85	176	3.3	482	1	US-07-792-885A-1	Sequence 1, Appl
86	176	3.3	482	2	US-08-142-439A-7	Sequence 7, Appl
87	176	3.3	482	2	US-08-869-477-7	Sequence 7, Appl
88	175	3.3	474	1	US-08-453-742-2	Sequence 2, Appl
89	175	3.3	474	1	US-08-454-464-2	Sequence 2, Appl
90	175	3.3	474	1	US-08-453-222-2	Sequence 2, Appl
91	175	3.3	474	1	US-08-452-802-2	Sequence 2, Appl
92	174.5	3.3	514	4	US-09-370-098-2	Sequence 2, Appl
93	171.5	3.2	294	1	US-08-142-439A-4	Sequence 4, Appl
94	171.5	3.2	294	2	US-08-869-477-4	Sequence 4, Appl
95	171	3.2	431	2	US-08-538-816A-9	Sequence 9, Appl
96	171	3.2	431	4	US-09-076-651-9	Sequence 9, Appl
97	171	3.2	431	4	US-09-208-394-9	Sequence 9, Appl
98	171	3.2	438	2	US-08-538-816A-1	Sequence 1, Appl
99	171	3.2	438	2	US-09-076-651-1	Sequence 1, Appl
100	171	3.2	438	4	US-09-208-394-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-08-956-322-4  
; Sequence 4, Application US/08956322  
; Patent No. 6277977  
; GENERAL INFORMATION:  
; APPLICANT: SATHE, GANESH  
; APPLICANT: MAO, JOYCE  
; TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES  
; TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,322  
; FILING DATE: 23-OCT-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/049,329  
; FILING DATE: 11-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70075  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 521 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-956-322-4

Query Match 9.4%; Score 501.5; DB 4; Length 521;  
Best Local Similarity 28.7%; Pred. No. 5.3e-32;  
Matches 155; Conservative 95; Mismatches 197; Indels 93; Gaps 19;

QY 398 LENQVL-QMEKALSLGSLPDLNAGEMINQVSRLLHSPDMLAPLAQRLLKVDDIGLQLN 456  
DB 12 LTNQVLNRTEGQEISSTATTILRDVESKVLTAIXDPE-----QKVLKIQND----- 59  
QY 457 FSNNTISLTSPSLALAIRVNASSFNNTTFVAODPANLQVSL-----ETQAP 503  
DB 60 -----SVAIEQTQAITDNGSEERKT-----FNLNVQMNSMDIRCSDFIIQGDTPG 103  
QY 504 ENSIGTITLPSSLMNLPADHMLASRQVNFETFPALFODPDSLNLISLTSYVSSSVAN 563  
DB 104 -SAIAFISYS-----LGNLIINATFEE-----EMDKKDQVYLSQVYSAAGCP 145  
QY 564 LTVRNLTNRVNTLKHINPSQDELTVRCVFDLGRNGRGG-WSDNCGSCVKDRRLNETIC 622  
DB 146 KRVSLRSKSVTLTFQHKVKTPTSTKKFCVYVW---KSTGQGSQWSRDGCFLLIHVNKSHITMC 202  
QY 623 TCSHLTSGVLLDLSTSVLPAPMAOMALTFTTYICGGLSSIFLSVTLTYIAFAEKIRRDYP 682

DB 203 NCSHLSFAVLMAITSQEDP-----VLTIVTVGLSVSLCLLALATFLLCRAIQNTST 258  
QY 683 SKILIQCAALLLNFLVLLDSWIALYKMGCLICISAVAFELHYELLYSFTWMGLEAFHMYL 742  
DB 259 S-LHLQLSLCLFLAHLFLVG--IDRTEPKVLCSSIIAGALHYLYLAFTWMLLEGVHLFL 315  
QY 743 AL--VKVENTVIRKYLKFCI--VGMGVPVAVVVTIITLITSPDNYGLSGYKGFPGNSPDDF 798  
DB 316 TARNLTVVNYSSINRLMKWIMEFVGVGVPVAVTVAISAASWPHLYGTA-----DR 364  
QY 799 CWINNAVYFIVVGVFCVIFLLNYSMFIVLVOLCRKKKKQKOLGAORQTSIQDLRSIA- 857  
DB 365 CWLHLDQGFMSFLGVCFAIFSANLVLFLVFWILKR--KLSSLNSEVST-IQNRMLAF 421  
QY 858 ---GLTFLLGITGWFAPFAFGVNVVTFMVLFAFNLTLOGFFIFFYCVAKENVKQWRRY 914  
DB 422 KATAQLFILGCTWCLGLLQVGPAQVMAYLFTIINSLOGFFIFLVYCLLSQOVOKQKXW 481

RESULT 2  
US-08-956-322-2  
; Sequence 2, Application US/08956322  
; Patent No. 6277977  
; GENERAL INFORMATION:  
; APPLICANT: SATHE, GANESH  
; APPLICANT: MAO, JOYCE  
; TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES  
; TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,322  
; FILING DATE: 23-OCT-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/049,329  
; FILING DATE: 11-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70075  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 652 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-956-322-2

Query Match 9.4%; Score 501.5; DB 4; Length 652;  
Best Local Similarity 28.7%; Pred. No. 7.6e-32;  
Matches 155; Conservative 95; Mismatches 197; Indels 93; Gaps 19;

QY 398 LENQVL-QMEKALSLGSLPDLNAGEMINQVSRLLHSPDMLAPLAQRLLKVDDIGLQLN 456  
DB 12 LTNQVLNRTEGQEISSTATTILRDVESKVLTAIXDPE-----QKVLKIQND----- 59  
QY 457 FSNNTISLTSPSLALAIRVNASSFNNTTFVAODPANLQVSL-----ETQAP 503  
DB 60 -----SVAIEQTQAITDNGSEERKT-----FNLNVQMNSMDIRCSDFIIQGDTPG 103  
QY 504 ENSIGTITLPSSLMNLPADHMLASRQVNFETFPALFODPDSLNLISLTSYVSSSVAN 563  
DB 104 -SAIAFISYS-----LGNLIINATFEE-----EMDKKDQVYLSQVYSAAGCP 145  
QY 564 LTVRNLTNRVNTLKHINPSQDELTVRCVFDLGRNGRGG-WSDNCGSCVKDRRLNETIC 622  
DB 146 KRVSLRSKSVTLTFQHKVKTPTSTKKFCVYVW---KSTGQGSQWSRDGCFLLIHVNKSHITMC 202  
QY 623 TCSHLTSGVLLDLSTSVLPAPMAOMALTFTTYICGGLSSIFLSVTLTYIAFAEKIRRDYP 682

Db 961 stlllvndcsvhasngnasterngvsfsvqgdvclhdfgkghmfnekedscngkgr 1020

Qy 1021 MALRRTSKRGLHFIQOM 1038

Db 1021 malrtrskrgslhfiqom 1038

RESULT 2

AA01247

ID AAB01247 standard; Protein; 1013 AA.

XX AC AAB01247;

XX 03-OCT-2000 (first entry)

DE Human HE6 receptor.

XX Human: HE6 receptor; zsig56; seven transmembrane domain receptor; hypotensive; antigout; cytostatic; antiinflammatory; ion homeostasis; cardiant; neurotransmitter; neuroprotective; antiparkinsonian; cerebroprotective; nootropic; neuroleptic; tranquiliser; antiarthritic; reproductive; signal transduction activator; bone disease; hypertension; renal failure; heart failure; hyperthyroidism; hyperparathyroidism; carcinoma; sarcoidosis; pancreatitis; stress; high blood pressure; immune depression; periodontal disease; neurodegenerative disease; multiple sclerosis; Alzheimer's disease; Parkinson's disease; schizophrenia; manic depression; stroke; rheumatoid arthritis; male fertility; spermatogenesis stimulation; pregnancy regulation; prostate cancer.

XX OS Homo sapiens.

XX PN WO20003473-A2.

XX PD 15-JUN-2000.

XX PF 02-DEC-1999; 99WO-US28492.

XX PR 10-DEC-1998; 98US-0208691.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Sheppard PO, Ellsworth JL;

XX DR WPI; 2000-442164/38.

XX PT Novel G-protein coupled receptor zsig56 useful for treating hypertension, hyper and hypothyroidism, inflammation, gout, carcinoma, pancreatitis, Alzheimer's disease and Parkinson's disease, renal and heart failure.

XX PS Disclosure; Fig 1; 121pp; English.

XX The present sequence is the human HE6 receptor, which shows homology to a seven transmembrane domain receptor designated zsig56. The full length nucleotide sequence was obtained from a human retina library. zsig56 polypeptides, nucleic acid, agonists and/or antagonists may be used to treat a wide range of disorders including certain bone diseases, hypertension, renal failure, gout, congestive heart failure, hyperthyroidism, hyperparathyroidism, certain carcinomas, sarcoidosis and pancreatitis. They can be used to treat disorders associated with changes in ion or electrolyte homeostasis, and stress induced disorders such as high blood pressure, heart failure, immune depression and periodontal disease. They may be used to treat neurodegenerative diseases, including multiple sclerosis, Alzheimer's disease and Parkinson's disease, schizophrenia and manic depression, and to repair nerve tissue following damage due to strokes and brain and spinal injuries. Inflammatory disorders such as rheumatoid arthritis can also be treated. zsig56 is expressed in tissues associated with reproduction, i.e. the testis, prostate and placenta, and may be used to treat male fertility by stimulating spermatogenesis and to regulate gestation and birth. zsig56 may be useful as a marker or therapeutic agent in the treatment of prostate cancer.

XX Sequence 1013 AA;

Qy 25 MVSFVRCQGHVGRTEVLLFKFLVLIICLHVLTSLSEEDTNSLSLPPAKLSVVSFA 84

Db 1 mvfsvrgcghvgrteevlltfkflvliiclhvltslseedtndsslsppaklsvvsfa 60

Qy 85 PSSNEVETTSLLNDVTLSSLPSNETEKTITVKTENASGVKPKPORNICNLSSICNDSAFPR 144

Db 61 pssnevettsslndvttllsslpnetektktivkfnsagvkvprnrcnlssicndsafr 120

Qy 145 GEIMFYDKESTVPQNOHITNGTLTGVLSELKRSSELNKTQLTSETYFFIMCATAEAGS 204

Db 121 geimfydkestvpqnhitngtlgtvlselkrseinkltqitsetyffimcataeags 180

Qy 205 TLNCTFTIKLNTMNAACAATAALERVKIRMEHCCSVRIPCSPPEELGKLCQDQDPI 264

Db 181 t-nctftiklntmnacaaalalervkirmehccsvrircpspeelgklqcdlqdpi 239

Qy 265 VCLADHPRGPPFPSSQSIPVPRATVLSQVPKATSFAPPPDYSPVTHVPSPIGEOPLS 324

Db 240 vcladhprgppfssqsipvpratvlsqvpkatsfaepdyspvthvpspiqeipls 299

Qy 325 POPSAPIASSPAIDMPPQSETISSPMQTHVSGPPPVKASFSSPTVSAPANVNTTSAPP 384

Db 300 ppsapiasspa idmppqsetisspmqthvsgtpppvkasfsaptvsapanvnttsapp 359

Qy 385 VGTDIVNTSSISLENOVLQMEKALSGLEPNLAGEMINOVSRLLHSPDMLAPLQRL 444

Db 360 vgtdivntssislenovlqmekalsglepnlageminqvrrllhspddmlaplqrl 419

Qy 445 LKVVDDIGLQNFNTTISLTPSLALAVIRVNASSFNTTFFAQDPAVLQVLETAPE 504

Db 420 lkvvddigqlnfnttisltspslalavirvnassfnttffvaqdpavlnvletpaqe 479

Qy 505 NSIGITTLPSLLMNLPAHDMELASRVQNFETPALFQDPSLENLSISVIVSSVANL 564

Db 480 nsigitltpssllmnlpahd melasrvqnfetpal fqdpslenlsisvissvanl 539

Qy 565 TVRNLTRNVTVTLKHINPQDELTVRVCFWDLGRNGRGWSDNGCSVKDRRLNETICTC 624

Db 540 tvrnltrnvtvltkhinpsqdeltrvcvfdlgrngrgwsgdngcsvkdrrlnetictc 599

Qy 625 SHLTSEFVLLDLSTRSVLPAQMMLTFITVIGCGLSIFISVTLVTVIAFEKIRRDYPSK 684

Db 600 shltsefvllldlstrsvlpaqmmaltfityigcglssifisvltvtyiafekirrdypsk 659

Qy 685 ILIQCAALLLNVLFLDLSWIALYKMOGLCISVAVFLHYFVLLVFTWMGLEAFHMYIAL 744

Db 660 lliqlcaalllnvflldswialykmqglcisvavflhyflvftwmgleafhmyial 719

Qy 745 VKVFNTYIRKYILKFCIVGWGPVAVVVTIITLISPONVGLSGYKFPNGSPDDFCWINNN 804

Db 720 vkvntfyrkyil kfcivgwgpavvvvtiiltispdnyglsgykgfngspddfcwinnn 779

Qy 805 AVFYITVGVYFCVIFLLNVSMFIVLVQLCRKKKQKOLGAQRKTSIQDLRSIAGLFTLLG 864

Db 780 avfyitvgyfcvifllnvsmfivlvqlcrkkkqlgaqrktsiqdlrsiagltfllg 839

Qy 865 ITWGAFFAWGPVNVTFMYLFAIENTLOGFFIFFYCVAKENVRKQRRYLCGCKLRALAE 924

Db 840 itwgaaffawgpvnvtfmylfaifntlqgffiffyvcakenvrkqrrylcogcklr lae 899

Qy 925 NSDMSKTATNGLKKQTVNQGVSSSSSNSLQSSNSTNTTLLVNNDCSVHASGNGNASTER 984

Db 900 nsdmsktatnglkkqtvnqgvssssnslqssnstnttllvnndcsvhasngnaster 959

Qy 985 NGVSFVQNGDVCLHDFGKGHMFNEKEDSCNGKGRNALRRTSKRGLHFIQOM 1038

960 ngvsvqngdvclhdfgkghmnekcdscngkgrmalrrtskrgslhlfiegm 1013  
|||||  
RESULT 3  
ID AAM24057 standard; Protein: 328 AA.  
AC AAM24057;  
DT 12-OCT-2001 (first entry)  
XX Human EST encoded protein SEQ ID NO: 1582.  
DE Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition.  
XX Homo sapiens.  
OS WO200154477-A2.  
PN 02-AUG-2001.  
XX 25-JAN-2001; 2001WO-US02687.  
XX 25-JAN-2000; 2000US-0491404.  
PR 17-JUL-2000; 2000US-0617746.  
PR 03-AUG-2000; 2000US-0631451.  
PR 15-SEP-2000; 2000US-0663870.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX WPI: 2001-476164/51.  
DR N-PSDB: AAH98716.  
XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
PT antibodies and research use -  
PS Claim 20; Page 1081-1082; 1275pp; English.  
XX The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a  
CC protein of the invention.  
XX Sequence 328 AA;  
SQ  
Query Match 32.5%; Score 1739; DB 22; Length 328;  
Best Local Similarity 100.0%; Pred. No. 1.3e-120;  
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 711 MGLGISVAVFLHYFLVSVFTWGLEAFHMYLALVKVFNFTYIRKYILKFCIVGVGPAVV 770  
Db 1 mglgisvavflhyflvsvftwgleafhmylalkvkfntyirkyilkkfcivgvgpavv 60  
QY 771 VTILITISPDNYGLSGYKFPNGSPDDFCWNNNAVFTYITVGVYFCVIFLLNYSMEIWL 830  
Db 61 vtilitispdnyglsgykgfngspddfcwinnnavfytvgyfvcvifllnysmfivl 120  
QY 831 VOLCRIRKKKQLGAQRKTSIODLRSTAGLTFLGITWGFAFFAWGPNVFTMYLFAFNT 890  
Db 121 vqlcrirkkkqlgaqrktsiodlrstagiitflgitwgfaffawgpnvntfmylfaifnt 180

891 LOGFFIIFCYVAKENVRKOWRRYLCCGKRLAENSDWSKTATNGLKOTVNOGVSSSN 950  
|||||  
Db 181 lqgffifcyvakenvrkqwrrylccgkrlaensdwsktatnnglkkqtvnqgvsssn 240  
QY 951 SLOSSNSTSTTLVNNDCSVHASGNGNASTERNVGSFVSQNGDVCVLDHFTGCKQHMFNE 1010  
|||||  
Db 241 slqssnststtlvnndcsvhasgngnasternvgsfvsqngdvclhdfgkghmfne 300  
QY 1011 KEDSCNGKGRMALRRTSKRGSLHFIETQM 1038  
|||||  
Db 301 kedsngkgrmalrrtskrgslhlfiegm 328  
RESULT 4  
ID AAU00195 standard; Protein: 1220 AA.  
XX AAU00195;  
XX 12-SEP-2001 (first entry)  
XX Human novel G-protein coupled receptor, NGPCR#6.  
DE Human; novel G-protein coupled receptor; NGPCR: antagonist;  
KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
KW abnormal blood pressure; cancer.  
XX Homo sapiens.  
OS WO200118207-A1.  
PN 15-MAR-2001.  
XX 08-SEP-2000; 2000WO-US24591.  
XX 10-SEP-1999; 99US-0153366.  
PR 15-NOV-1999; 99US-0165510.  
XX (LEXI-) LEXICON GENETICS INC.  
XX Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
PI Sands AT;  
XX WPI: 2001-191773/19.  
DR N-PSDB: AAS00115.  
XX New nucleic acids encoding human G-protein coupled receptors, useful as  
PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
PT disease and cancer -  
XX Disclosure; Page 78-80; 149pp; English.  
XX The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
CC The NGPCRs are members of the 7 transmembrane domain class of  
CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
CC them and (ant)agonists of the NGPCRs are useful for the treatment  
CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
CC disease, abnormal blood pressure, cancer and any associated symptoms.  
XX Sequence 1220 AA;  
SQ  
Query Match 27.0%; Score 1446; DB 22; Length 1220;  
Best Local Similarity 35.4%; Pred. No. 4.4e-98;  
Matches 365; Conservative 183; Mismatches 330; Indels 154; Gaps 35;  
QY 68 NSSLSPPAKLSVVSFAPSNE---VETTSINDVTLSLLPSNETEKTKITIVKTFNAGSV 124  
Db 233 nmal---pvkekedifaesfeqlcvwnslgsvgnkrnyetvpodstisk-----v 283  
QY 125 KPQRNTCNLSICNDSAFFRGEIMFQYDKESTVPQNOHITNGTLTGVLSELKPSLNK 184  
Db 284 ibpgnkllilgnsnqncivslkgdi-----ynfrlwnftmaki-lsnlscnvkn 331



QY 407 KALSLS-LSLEPNLAGEMINQVSRLLHSPDMLAPLAQRLLKVVDDIGLQNFNTT-LSL 464  
 Db 615 rivnkeeniditlgtlmnifslssdsdlessealktidelafkidlnstshvni 674  
 QY 465 TSPSLALAVIRVNASSFTTFFVAQDPAN-...LQVSLQAPENSIGTITLPSLMMNL 520  
 Db 675 ttrnlalsvslpgtnaisnfsiglpnnesyfgmdfes-gqvdpasvilppnllenl 733  
 QY 521 PAHDMELASRVQNFETFPALFQDPSLENLSLSYVSSSVANLTVRNLTNRVTVLKHI 580  
 Db 734 spedsvlvrragftfnktglfdvgpqrktlvsymacsignitignikdpvgikikt 793  
 QY 581 NPSODELTVCVFDLGRGGSDNGC-SVKDRRLNETICTCSHLTSGVLLDLSRT 639  
 Db 794 rtqevhpi-cafwdlnknksfggwntsgcvahrdsdasetvclcnhthfgyldmlprs 852  
 QY 640 -SVLPAQ-MMALTFITYIGCGLSIFLSVTLVYIAFEKIRRDYPSKILFOLCAALLLN 697  
 Db 853 asqldarntkvlftisyigcgisaifsaatlityvafeklrdrdypskilmnllstallfn 912  
 QY 698 LVFLDLSHIALYKMOGLICISNAVFHYFLVLLSFTWMGLEAFHMYLALVKVFNTRYIRKYL 757  
 Db 913 lflldgwitsfnvdglciavavllhffllatftwmgleahmyialvkvfntryiryl 972  
 QY 758 KFCIVGCVPAVWVTIILTISPDN--YGLGSYKFPNGSPDDFCWINNNNAVFIYTVVGYF 815  
 Db 973 kfcigwglpalvsvvlasrnnnnyvkesyvk---ekgdefcwigdpvifvycagf 1029  
 QY 816 CVIFLLNVSMFIVLVQLCRKIKKOLGQAORTSIODLSRIAGLTLLGTWGFAPFANG 875  
 Db 1030 gvmfllniamfivmvqicgrngkrnsrlreevlnrlsvvsltflimgtwgfaffaw 1089  
 QY 876 PVNVTEMVLEAFNTLOGFFIFCYCAKENVKQWRRYLCCGKRLAENS DSKTATNG 935  
 Db 1090 plnlpfmylfafnsiqglfifhcamkenvqkwrhlccgfrflladnsdsktati 1149  
 QY 936 LKQTVNGVSSSSSLSQSSS-----NSTNSTLLVNNDSCSVHAGSNGNASTERNVGF 989  
 Db 1150 ikkasdnlgkslssssignsnyltskskssttyfkrn-----shtdnvsyeh---sf 1200  
 QY 990 SVQNGDV--CLH 999  
 Db 1201 n-kagslrqcfh 1211  
 RESULT 6  
 AAU00199 standard; Protein; 1221 AA..  
 AC AAU00199;  
 XX AAU00199;  
 DT 12-SEP-2001 (first entry)  
 XX Human novel G-protein coupled receptor, NGPCR#10.  
 DE Human; novel G-protein coupled receptor; NGPCR; antagonist;  
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
 KW abnormal blood pressure; cancer.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO200118207-A1.  
 PN 15-MAR-2001.  
 XX 08-SEP-2000; 2000WO-US24591.  
 XX 10-SEP-1999; 99US-0153366.  
 PR 15-NOV-1999; 99US-0165510.  
 XX (LEXI-) LEXICON GENETICS INC.  
 PA 99US-0165510.  
 XX

PI Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
 PI Sands AT;  
 XX WPI; 2001-191773/19.  
 DR N-PSDB; AAS00119.  
 XX New nucleic acids encoding human G-protein coupled receptors, useful as  
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
 PT disease and cancer.  
 XX Disclosure; Page 91-93; 149pp; English.  
 XX The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
 CC The NGPCRs are members of the 7 transmembrane domain class of  
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
 CC them and (ant)agonists of the NGPCRs are useful for the treatment  
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
 CC disease, abnormal blood pressure, cancer and any associated symptoms.  
 XX Sequence 1221 AA;  
 SQ  
 Query Match 27.0%; Score 1446; DB 22; Length 1221;  
 Best Local Similarity 35.4%; Pred. No. 4.4e-98;  
 Matches 365; Conservative 183; Mismatches 330; Indels 154; Gaps 35;  
 QY 68 NSSLSPPPAKLKSVSPAPSSNE---VETSLNDVTLSSLPSNETKTKITIVKTFNSGV 124  
 Db 234 mnal---pvkekedifaesfedqiclvwnslsgisgvnfrknyetvpcdstisk-----v 284  
 QY 125 KPCNICNLSSICNDGAPFGEIMFOYDKESTVPQNOHIHTNGTLTGLVLSLSELKRSELNK 184  
 Db 285 lpgnkliligsnqneivslkgdi-----yfrlwnftmaki-lanlsncvkg 332  
 QY 185 TLQTLSETVFIMCATAEAOSTLNC-TFTIKLNT-MNACAAIAALERVKIRPMEHCCSV 242  
 Db 333 vvdgndfwnlpnlalkaesnlscgyliplaaelascadigtl-----cqv 382  
 QY 243 RIPCPSPEELKQCLQDLPVCLADHPR--GPPFSSS---QIPVVPVATVLSQVPR- 296  
 Db 383 nspsttpvtvtnm-----pvtndrkgrndgilyrsvvignlilrhpevkvskaev 436  
 QY 297 ATSFAPEDPDYSPVTHNV-----PSPIGEIOPLSPOP----- 327  
 Db 437 lnstfgwnyvtvyvvnisfhlsagedkikvksledeprlvllwallynatntnlegki 496  
 QY 328 --SAPIASSPAIDMPQSETIS-----SPMQTHVSGTTPPVKASF 366  
 Db 497 lqgklknnesiddegirhltnvvrqighclameepkgyvpsiqpsev--lpcdkpgf 554  
 QY 367 S-----SPTVS--APANVT--TSAPPVQTDVNTS-----SISLENOVLQME 406  
 Db 555 sasricfynatnplvtvgpvdiscikeanevanqilnitadggnitsanitaveqvk 614  
 QY 407 KALSLS-LSLEPNLAGEMINQVSRLLHSPDMLAPLAQRLLKVVDDIGLQNFNTT-LSL 464  
 Db 615 rivnkeeniditlgtlmnifslssdsdlessealktidelafkidlnstshvni 674  
 QY 465 TSPSLALAVIRVNASSFTTFFVAQDPAN-...LQVSLQAPENSIGTITLPSLMMNL 520  
 Db 675 ttrnlalsvslpgtnaisnfsiglpnnesyfgmdfes-gqvdpasvilppnllenl 733  
 QY 521 PAHDMELASRVQNFETFPALFQDPSLENLSLSYVSSSVANLTVRNLTNRVTVLKHI 580  
 Db 734 spedsvlvrragftfnktglfdvgpqrktlvsymacsignitignikdpvgikikt 793  
 QY 581 NPSODELTVCVFDLGRGGSDNGC-SVKDRRLNETICTCSHLTSGVLLDLSRT 639  
 Db 794 rtqevhpi-cafwdlnknksfggwntsgcvahrdsdasetvclcnhthfgyldmlprs 852  
 QY 640 -SVLPAQ-MMALTFITYIGCGLSIFLSVTLVYIAFEKIRRDYPSKILFOLCAALLLN 697  
 Db 853 asqldarntkvlftisyigcgisaifsaatlityvafeklrdrdypskilmnllstallfn 912

Qy 698 LVFLDLSWIALYKMOGLCISVAVFLHYFLVSTWGMLEAFHMYLALVKVFNTYIRKYIL 757  
 Db 913 lllldgwitsfnvdlgciavavllhflfatftwmgleahmyialkvfntyril 972  
 Qy 758 KFCIVGWGPVAVVVTIILTSPDN--YGLSGYGFPPNGSPDDFCWINNAVYITVGVGF 815  
 Db 973 kfcilgwgipalvsvvlasrnnnevgyksgk--ekgdefcwqdpvifvtcagyl 1029  
 Qy 816 CVIFLNVSMFIVLVQLCRKKKQLGAQRKTSIQDLRSIAGTLFLGLITWGEFAFFAWG 875  
 Db 1030 gvmfflinamfivmvqicgrnkrntireevlnrlsvsvslflgltwgfafawg 1089  
 Qy 876 PNVTFMYLFAIFNTLOGFFIFIFCYVAKENVRKQWRRLCCGKRLAENSWSKTATNG 935  
 Db 1090 plnlpmylfsifnslqglfifhcamkenvqgwrhlccgrfrladnsdskstati 1149  
 Qy 936 LKKQTVNOGVSSNSLSQSS-----NSTNSTLLVNDSCVHASGNGNASTERNVGVF 989  
 Db 1150 lkkssdnlgkslssssignstlytskskssttyfkrn-----shdnvseyh---sf 1200  
 Qy 990 SVQNGDV--CLH 999  
 Db 1201 n-ksqslrqcfh 1211

RESULT 7  
 AAU00194  
 ID AAU00194 standard; Protein; 1249 AA.  
 AC AAU00194;  
 DT 12-SEP-2001 (first entry)  
 DE Human novel G-protein coupled receptor, NGPCR#5.  
 KW Human; novel G-protein coupled receptor; NGPCR; antagonist;  
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
 KW abnormal blood pressure; cancer.  
 OS Homo sapiens.  
 PN WO200118207-A1.  
 XX 15-MAR-2001.  
 PF 08-SEP-2000; 2000WO-US24591.  
 PR 10-SEP-1999; 99US-0153366.  
 PR 15-NOV-1999; 99US-0165510.  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
 PI Sands AT;  
 XX WPI; 2001-191773/19.  
 DR N-PSDB; AAS00114.  
 XX New nucleic acids encoding human G-protein coupled receptors, useful as  
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
 PT disease and cancer.  
 XX Disclosure; Page 74-77; 149pp; English.  
 PS The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
 CC The NGPCRs are members of the 7 transmembrane domain class of  
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
 CC them and (ant)agonists of the NGPCRs are useful for the treatment  
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
 CC disease, abnormal blood pressure, cancer and any associated symptoms.  
 XX Sequence 1249 AA;

Query Match 27.0%; Score 1446; DB 22; Length 1249;  
 Best Local Similarity 35.2%; Pred. No. 4.6e-98;  
 Matches 361; Conservative 185; Mismatches 332; Indels 148; Gaps 32;

Qy 68 NSSLSPPPAKLSVVSFAPSNE---VETTSINDVTSLLSPSNETEKTKITIVKTFNASGV 124  
 Db 233 onal---pvkekedifaesfeqlclvwnnslgsygnfkryetvpcdstisk-----v 283  
 Qy 125 KQORTNICNLISSONDSAFFRGEIMFOYDKESTVPOHQHITNGTLGVLSELKRSSELNK 184  
 Db 284 lpgngkllilgnsqneivslkgdi-----ynfzlnwftmbaki-lsnlscnvkgn 331  
 Qy 185 TLQTLSETFIMCATAEAQSTLNC-TETIKLNN-TMNAACAATAALERVIRPMEHCCSV 242  
 Db 332 vvwqndfnwipnlaikaesnlscgsyllipaaelascadlgtl-----cgatv 381  
 Qy 243 RIPCPSSPEELGKLODQPIVCLADHPR--GPPFSSS---QSIPVVVPRATVLSQVPK- 296  
 Db 382 nspsttpptvttnm-----pvtndridkqndgilyrisvviqnllrhpekvqskvae 435  
 Qy 297 ATSPAEPPDPSPVTHNV-----PSPIGEIQPLSPQP----- 327  
 Db 436 lntftqwnytyvvnslsfhlsagedkikvkrsldeprlwlwallvynatnntnlegki 495  
 Qy 328 --SAPIASSPAIDMPPQSETIS-----SPMPQTHVSGTTPPVKASF 366  
 Db 496 lqqkilknnesideglrlhtcnvrqlghclameepkgyywpisqpsyv--lpcdkpgf 553  
 Qy 367 S-----SPTVS--APANVT--TSAPPVQTDIVNTS-----SISDLENQVLQME 406  
 Db 554 sasricfynatnplvtcywgpvdiscnclkeanevanqilnltadgqnltsanitniveqv 613  
 Qy 407 KALSL-GSELPNLAGEMINOVSRLLHSPDMLAPLQRLKLVVDIGLOLNSNTT-ISL 464  
 Db 614 rivnkeeniditlgstlmlnifsnlssdsdlessealktidelafakidninsthvi 673  
 Qy 465 TSPSLALAVIRVNASSEFNTTFVAQDPAN---LQVSLQAPENSIGNITLPSLSLMLN 520  
 Db 674 ttrnlalsvssllpgtnaisnfsiglpnncesyfmdfes-gqvdpiaasvilppnlienl 732  
 Qy 521 PAHDMELASRVQNFETPALFQDPSLENIISLISYIVSSSVANLTVRNLTNRVTVLKH 580  
 Db 733 spedsvlvrraqftfnktglfdvgpqrktlvsvvmacsignitignlkdpvqikht 792  
 Qy 581 NPSQDELTVRCVFWDLGRNGRGGSWNGC-SVDRRLNETICTCSHLTSFGVLLDLSRT 639  
 Db 793 rtqevhhpi-carwdlnknksfggwntsgcvahrdsasetvclcnhthfvgvldmldr 851  
 Qy 640 -SVLPAQ-MMALTFITYIGGLSSIFLSVTLVTYIAPEKIRRDYPSKILIQCAALLLN 697  
 Db 852 asqldarntkvltfisyigcgisaifsaatlityateklrrdypskilmnltallfin 911  
 Qy 698 LVFLDLSWIALYKMOGLCISVAVFLHYFLVSTWGMLEAFHMYLALVKVFNTYIRKYIL 757  
 Db 912 lllldgwitsfnvdlgciavavllhflfatftwmgleahmyialkvfntyril 971  
 Qy 758 KFCIVGWGPVAVVVTIILTSPDN--YGLSGYGFPPNGSPDDFCWINNAVYITVGVGF 815  
 Db 972 kfcilgwgipalvsvvlasrnnnevgyksgk--ekgdefcwqdpvifvtcagyl 1029  
 Qy 816 CVIFLNVSMFIVLVQLCRKKKQLGAQRKTSIQDLRSIAGTLFLGLITWGEFAFFAWG 875  
 Db 1029 gvmfflinamfivmvqicgrnkrntireevlnrlsvsvslflgltwgfafawg 1088  
 Qy 876 PNVTFMYLFAIFNTLOGFFIFIFCYVAKENVRKQWRRLCCGKRLAENSWSKTATNG 935  
 Db 1089 plnlpmylfsifnslqglfifhcamkenvqgwrhlccgrfrladnsdskstati 1148  
 Qy 936 LKKQTVNOGVSSNSLSQSS-----NSTNSTLLVNDSCVHASGNGNASTERNVGVF 989  
 Db 1149 lkkssdnlgkslssssignstlytskskssttyfkrn-----shdnvseyh---sf 1202

QY 990 SVONGD 995  
 Db 1203 ahadgd 1208

RESULT 8  
 AAU00190  
 ID AAU00190 standard; Protein; 1250 AA.  
 AC AAU00190;  
 XX  
 DT 12-SEP-2001 (first entry)  
 DE Human novel G-protein coupled receptor, NGPCR#1.  
 KW Human; novel G-protein coupled receptor; NGPCR; antagonist;  
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
 KW abnormal blood pressure; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200118207-A1.  
 XX  
 XX 15-MAR-2001.  
 XX  
 XX 08-SEP-2000; 2000WO-US24591.  
 XX  
 XX 10-SEP-1999; 99US-0153366.  
 PR 13-NOV-1999; 99US-0165510.  
 XX  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX  
 XX Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
 PI Sands AT;  
 PI  
 XX WPI; 2001-191773/19.  
 DR N-PSDB; AAS00110.  
 XX  
 XX New nucleic acids encoding human G-protein coupled receptors, useful as  
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
 PT disease and cancer -  
 XX  
 PS Claim 2; Page 61-64; 149pp; English.  
 XX  
 CC The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
 CC The NGPCRs are members of the 7 transmembrane domain class of  
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
 CC them and (ant)agonists of the NGPCRs are useful for the treatment  
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
 CC disease, abnormal blood pressure, cancer and any associated symptoms.  
 XX  
 SQ Sequence 1250 AA;

Query Match . 27.0%; Score 1446; DB 22; Length 1250;  
 Best Local Similarity 35.2%; Pred. No. 4.6e-98;  
 Matches 361; Conservative 185; Mismatches 332; Indels 148; Gaps 32;

QY 68 NSSLSPPAKLSVSVFAPSNE---VETSLNDVTLSLPSNETETKTIIVKTFNASGV 124  
 Db 234 nnaal---pvkedidfaesfegclclvwnnslgsvgnfrknyetvpcdstisk-----v 284  
 QY 125 KPQRNICLSICNDASFRPGEIMFOYDKESTVPQOHTINGTLTGVLISLSELKRSSELNK 184  
 Db 285 ipngaklllgsnqnaisvlkgdi-----ynfriwnftmnnaki-lsnlscnvkgn 332  
 QY 185 TLQTLSEYTFIMCAFAEAGOSTLNC-TFTTKLNN-TNACAAIAALERVKIRPMEHCOCVS 242  
 Db 333 vvdwqndfwnlpnalkaesnlscgsvlylplpaaelascadlgtl-----cqatv 382  
 QY 243 RIPCSPSEELGLKLOCDLPDVLCLADHPR--GPPSSS---OSIPVPRATVLSQVPK- 296

Db 383 nspsttpptvttnm-----pvtnrldkgrndgilyrisvviqnrlhrhpevkqskvaev 436  
 QY 297 ATSAEPDPDYSPVTHNV-----PSPICEIOLPSQP----- 327  
 Db 437 lnstfgwnyvtvyvvnisfhlsgedkikvksrledeprlvllwallyvnnatnntnlegki 496  
 QY 328 --SAPIASSPAIDMPPQSETIS-----SPMPQTHVSGTTPPVKASPF 366  
 Db 497 igqklknnesideglrlhtvnnvrlghclameepkgyvwpisqpsyev--lpcdpkpgf 554  
 QY 367 S-----SPTVS--APANVT--TSAPPVQTDIVNTS-----SIDLENOVLQME 406  
 Db 555 sasricfynatnplvtvgvpsdnclkeanevanqlnitadgqnltsanitniveqvk 614  
 QY 407 KALSU-GSLEPNLAGEMINQVSRLLHSPDMLAPLQRLKLVVDDIGLQNFSTNT-ISL 464  
 Db 615 rivnkeeniditlgstlmifnlsissdsdliessaealktidelafkldnshvni 674  
 QY 465 TSPSLALAVIRVNASSFNNTTFFVAQDPAN----LQVSELTQAPENSIGTITLPSLMMNL 520  
 Db 675 ttrnlalsvssllpgtnaisnfsigipsnnesyfqmdfes-ggvdpilasvilppollenl 733  
 QY 521 PAHDMELASRVQFNPFETPALFQDPSLENLSLISYVSSVANLTVRNLTRNVTVTLKHI 580  
 Db 734 spedsvlvrarqdtfnktglfdvgppqrktlvsymacsignitignlkdpvgikikt 793  
 QY 581 NPSQDELTVRCVFWDLGRNGRGWSDNCG-SVKDRRLNETICTCSHLTSFGVLLDLSRT 639  
 Db 794 rtqevhhpi-cafdwlnknksfggwntsgcvahrdsdasetvelcnhftghgvmldprs 852  
 QY 640 -SVLPAQ-MMALTFITYICGLSSIFLSVTLVYIAFEKIRRDYPSKILQICALLLN 697  
 Db 853 asqldarntkvtfsyigcisaifsaatlityavafekrrdypskilmlnlsallfin 912  
 QY 698 LVFLDLSWTALYKMOGLCISVAVFLHYFLVSTWMLGFAFMYLALVKVENTYIRKYL 757  
 Db 913 lflldgwitsfnvdlciaavallhflfllatftwmlglaahmyialvkvfntyril 972  
 QY 758 KFCIVGWGPAVVVVTITISPDN--YGLGSYKGFPPNGSDDFCWINNNAVYITVGVYF 815  
 Db 973 kfciigwipalvsvvlasrnanevygkesygk--ekgdefcwigdpvifvvtcagvf 1029  
 QY 816 CVIFLLNVSMFIVLVOLCRKKKQKOLGAOKTSDIOLRSTAGLTGTLGTWGAFFAWG 875  
 Db 1030 gvmfllamfivmvgicgrngkrnsrtlrvevlnrsvslfllgmctwgfaffaw 1089  
 QY 876 PVNVTFMYLFAIFNTLQGFIFIFYCVAKENVRKQWRYCCGKRLAENSWSKATNG 935  
 Db 1090 plnifmylfsifnslqgifiifhcamkenvqkqrhccgrfrladsnswktatni 1149  
 QY 936 LKKQTVNQGVSSSSNSLQSSS-----NSTNTLLVNNDCSVHASGNNGNASTERNGVSF 989  
 Db 1150 ikkssdnlgkslssssisgnstlytsksssttyfkrn-----shtdsasmdkslskl 1203  
 QY 990 SVONGD 995  
 Db 1204 ahadgd 1209

RESULT 9  
 AAU00198  
 ID AAU00198 standard; Protein; 1250 AA.  
 AC AAU00198;  
 XX  
 DT 12-SEP-2001 (first entry)  
 DE Human novel G-protein coupled receptor, NGPCR#9.  
 KW Human; novel G-protein coupled receptor; NGPCR; antagonist;  
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
 KW abnormal blood pressure; cancer.  
 XX



PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
 PT disease and cancer -

XX Disclosure; Page 121-123; 149pp; English.

XX The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
 CC The NGPCRs are members of the 7 transmembrane domain class of  
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
 CC them and (ant)agonists of the NGPCRs are useful for the treatment  
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
 CC disease, abnormal blood pressure, cancer and any associated symptoms.

XX Sequence 1192 AA;

Query Match 27.0%; Score 1444.5; DB 22; Length 1192;  
 Best Local Similarity 34.8%; Pred. No. 5.5e-98;  
 Matches 354; Conservative 177; Mismatches 293; Indels 193; Gaps 33;

QY 65 DTNSSLSPPPAKLSVSWFAPSSNEVETSLNDVTLSLLPSNETEKTKITIVKTFNAGS- 123  
 DB 277 dstiskvpgngklll-----gsnqeivskgdynfrlwnftmnaakilsnscvkn 331  
 QY 124 -----VKPQNI-----CNLSSICNDSAFFRGEIMFQY 151  
 DB 332 vvdwgnfdwnipnialkaesnlscgsyllipaaelaascadglcqdgiyrisvviq- 390  
 QY 152 DKESTVPQNHITNGLTGVLSLSELRSE----LNKTLQTLSETYFIMCATAEQAOSTL 206  
 DB 391 -----nllrhpevskvskvaewlnstfqwnvtyv-----v 422  
 QY 207 NCTFTIKLNTMNACAAIAALRVKIRMEHCCSVRIPCSPSEELGKL----- 256  
 DB 423 nisthls-----agedkikvk-----rsledeprlvwallvyna 457  
 QY 257 --QCQLODPVCLADHPGPPSSQSIWVPRATVLS--QVPKATSFAPPPDPSPVTHN 312  
 DB 458 tntnlegkll-----qgkilknesldegrlhtvvnvqrlghclameepkgy-----y 506  
 QY 313 VPSPIGETOP---LSQPQSAPIASSPAIDMPPQSETISSPMPQTHVSGTPPVKASFS 369  
 DB 507 wps-----lpseyvlpcdkpqsasri-----cfynatnplv----- 540  
 QY 370 TVSAPANVT--TSAPPVQTDIVNTS-----SISLENOVLQMEKALSL-GSLEPNLAG 420  
 DB 541 tywgvdisnclkeanevangilnltadgpnltasnitniveqkriknkeeniditlgs 600  
 QY 421 EMINQSVRLHSPDMLAPLAORLLKVDDIGLQNFNTT-LSLTSPLALAVIRYNAS 479  
 DB 601 tlmlfnillsdssdllesseaiktidelafkldlnstshvntnrlalsvssllpg 660  
 QY 480 SFNTTTFVAQDPAN---LOVSELOAPENSIGTITLPSLSMNNLPAHDMELASRVQNF 535  
 DB 661 tnaissfiglpsnnesyfqmdfes-gvdpbiasvilppnllenlspeidsvlvraqftf 719  
 QY 536 FETPALFQDPSLENLSLSYVSSVANLTVRNLTRNVTLRKHINPSQDELTVRCVFW 595  
 DB 720 fntkglqfdvqprkrlsvymacsignitgnkqpvqikikhtqevhhpi-catwd 778  
 QY 596 LGRNGRGCGSDNGC-SVKDRRLNETICTSHLTSFGLVLLDLSRT-SVLPQAQ-MMALTFI 652  
 DB 779 lnkksfggwntsgcvahrdasatvcclnftthfgvldmldprsasqldarntkvtlfi 838  
 QY 653 TYIGGLSSIFLSVTVVYIAPEKRRDPYRSKILQICLALLNLVFLDLSWIALYKMQ 712  
 DB 839 syigcgaisaifaatllyvafekirrdypskilmstallfnllfldgwitsfnvd 898  
 QY 713 GLCISAVFLHYFLVSTWMLGAFHMYALVVKVFNTRYKYLKFCIVGWGVPVAVVT 772  
 DB 899 glciavallhflattfwmglesahmyialvkvntyriryllkfcilgwigpalvvs 958  
 QY 773 ILITISPDN---YGLGSYKGFPGNSPDDFCWNNNAVXYITVVGFCVIFLLNVMFVLVL 830

DB 959 vvlasrnnnevgykesygk---ekgdefcwldpvlvyvtcagfygmflniamfiwv 1015  
 QY 831 VOLCRIRKKKQOLGAORKTSTIODLRSTAGTLTFLIGITWGAFFAWGPVNVTFMYLFAIFNT 890  
 DB 1016 vqicgrngkrsnrtlreevlnrlsvsltilgmwtgaffawgpinipfmylifsins 1075  
 QY 891 LQGFIFIFCYCAKENVRKQWRYLCCGKRLAENSDWSTATNGLKKQTVNQGVSSSSN 950  
 DB 1076 lqgifiifhcamenvqkwrhlcocgrfrladnsdwsktatnllkssnllgkslss 1135  
 QY 951 SLOQSS-----NSTNSTLLVNDSCVHAGNASTERNGVSVFQVQNDV--CLH 999  
 DB 1136 sigsnstylltsksssttyfkrn-----shtdnvsyeh----sfn-ksgsrlrqcfh 1182

RESULT 11

AAU00719  
 ID AAU00719 standard; Protein: 1192 AA.

XX AAU00719;  
 DT 12-SEP-2001 (first entry)  
 XX Human novel G-protein coupled receptor, NGPCR#29.  
 XX Human; novel G-protein coupled receptor; NGPCR; antagonist;  
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
 KW abnormal blood pressure; cancer.

OS Homo sapiens.

XX WO200118207-A1.

PD 15-MAR-2001.

XX 08-SEP-2000; 2000WO-US24591.

XX 10-SEP-1999; 99US-0153366.

PR 15-NOV-1999; 99US-0165510.

XX (LEXI-) LEXICON GENETICS INC.

XX Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;

PI Sands AT;

XX WPI; 2001-191773/19.

DR N-PSDB; AAS00138.

XX New nucleic acids encoding human G-protein coupled receptors, useful as  
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
 PT disease and cancer -

XX Claim 5; Page 141-145; 149pp; English.

XX The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
 CC The NGPCRs are members of the 7 transmembrane domain class of  
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
 CC them and (ant)agonists of the NGPCRs are useful for the treatment  
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
 CC disease, abnormal blood pressure, cancer and any associated symptoms.

XX Sequence 1192 AA;

Query Match 27.0%; Score 1444.5; DB 22; Length 1192;

Best Local Similarity 34.8%; Pred. No. 5.5e-98;

Matches 354; Conservative 177; Mismatches 293; Indels 193; Gaps 33;

QY 65 DTNSSLSPPPAKLSVSWFAPSSNEVETSLNDVTLSLLPSNETEKTKITIVKTFNAGS- 123

DB 277 dstiskvpgngklll-----gsnqeivskgdynfrlwnftmnaakilsnscvkn 331

QY 124 -----VKPQNI-----CNLSSICNDSAFFRGEIMFQY 151

Db 332 vvdwqndfwnipnlalkaesnlscgysylipipaaelascadlgticqdgiiyrisvviq- 390  
 Qy 152 DKESTVPQNHITNGTLTGVLSELKRS- LNKTLQTLSETYFTMCATAEAQSTL 206  
 Db 391 -----nlrhpevkqskvaewlnstfgwnyvtvyv-----v 422  
 Qy 207 NCTFTIKLNTMNACAAIAALERVKIRPMEHCCSVRIPCSPSPPEELGKL----- 256  
 Db 423 nlsfhls-----agedkikvk-----rsledeprlwallvyna 457  
 Qy 257 --QCLODQDIVCLADHPRGPPFFSSQSIPIVPRATVLS--QVPKATSAEPDPYSPVTHN 312  
 Db 458 tntnlnlegkili-----qqklklnesldeglrlhtvnrqlghclameepkgy-----y 506  
 Qy 313 VPSPIGEIOP---LSPQPSAPIASSPAIDMPPQSETISSPMPQTHVSGTPPPVKASFSSP 369  
 Db 507 wps-----iqpseyvlpcpdkpgfsasri-----cfynatnplv----- 540  
 Qy 370 TVSAPANVNT--TSAPPVQTDIVNTS-----SISDLENQVLOMEKALSL-GSLEPNLAG 420  
 Db 541 tywgpvdiscnlkeanevanqilntadgqnltsanitniveqvkriynkeeniditlgs 600  
 Qy 421 EMINQVSRLLHSPDMLAPLAQRLKLVVDIGLOLNFNTT- ISLTSPLALAVIRVNAS 479  
 Db 601 tlmnifsnlssdsdllessealktdelafklidlnstshvntitnlnalsvslp 660  
 Qy 480 SFNTTTFVAQDPAN---LOVSLTOAPENSIGTITLPSLSLMMNLPAMDMLASRVQNF 535  
 Db 661 tnaifnsglpennesyfmdfes-gvqdpiafslpnlentlenpsedsvlrraqftf 719  
 Qy 536 FETPALFQDPSLENLSIYSSIVSSVANLTNRNVTTLKHNPSODELTVRQVFW 595  
 Db 720 fktglfvgdqrktlsvymcasignitqnlkdpqikikhrtdqevhpi-cafed 778  
 Qy 596 LGRNGRGWSDNGC-SVKDRRLNETICTCSHLTSFGVLLDLSRI-SVLPAQ-MMALTFI 652  
 Db 779 lnkksfggwntsgcvahrdsasetvclcnhfchfgvldmldrpsasqldarntkvlfi 838  
 Qy 653 TYIGCGLSSIFSLVTLVTYIAFKIRDRDPSKILIQICAAALLLNLVFLDLSWIALYKMQ 712  
 Db 839 syigcgaisaifsaatltyvafeklrdrdpskilmnstaillnllfldgwitsfnvd 898  
 Qy 713 GLCISAVAFHLVFLVFTWGLAEAFHMYALVFNFTYIRKYILKFCIGVGVPAVVVT 772  
 Db 899 glciavavllhflfatftwmgleahmyialkvfntiirryilkfcligwlpalvvs 958  
 Qy 773 ILTITSPDN--YGLSGYGRPNCGSPDDFCWINNNAVFYITVVGVFCVIFLLNVSMFIVL 830  
 Db 959 vvlarnnnevgykesygk---ekgdefcwqdpvifvtcagyfvgvfflniafivm 1015  
 Qy 831 VOLCRIKKKQLGAORKTSTQDLRSIAGTLFLLGITWGFAPFANGPVNVTMYLFAIENT 890  
 Db 1016 vqicgrngkrnsrlreevlnrsvsltlfgmtwgfaffawgplnlpmylfsifns 1075  
 Qy 891 LOGFTIFCYCAKENVRQWRRYLCCGKRLAENSWSKATNGLKKQTVNQGVSSSN 950  
 Db 1076 lqglifliffcamkenvgqwrthlccgrlradnsdsktatnlikssdnlgsllss 1135  
 Qy 951 SLOQSS-----NSTNTSTLLVNDCSVHASGNAGNATERNGVSFVQNGDV--CLH 999  
 Db 1136 signstyltsksssttyfkrn-----shtdnvsyeh---sfn-ksgrlrcqfh 1182

RESULT 12  
 AAU00207  
 ID AAU00207 standard; Protein; 1193 AA.  
 XX  
 AC AAU00207;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Human novel G-protein coupled receptor, NGPCR#18.

XX  
 KW Human; novel G-protein coupled receptor; NGPCR; antagonist;  
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
 KW abnormal blood pressure; cancer.  
 OS Homo sapiens.  
 XX  
 PN WO200118207-A1.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 08-SEP-2000; 2000WO-US24591.  
 XX  
 PR 10-SEP-1999; 99US-0153366.  
 PR 15-NOV-1999; 99US-0165510.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
 PI Sands AT;  
 XX  
 XX WPI; 2001-191773/19.  
 DR N-PSDB; AAS00127.  
 XX  
 PT New nucleic acids encoding human G-protein coupled receptors, useful as  
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
 PT disease and cancer  
 XX  
 PS Disclosure; Page 109-111; 148pp; English.  
 XX  
 CC The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
 CC The NGPCRs are members of the 7 transmembrane domain class of  
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
 CC them and (antagonists of the NGPCRs are useful for the treatment  
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
 CC disease, abnormal blood pressure, cancer and any associated symptoms.  
 XX  
 SQ Sequence 1193 AA;  
 Query Match 27.0%; Score 1444.5; DB 22; Length 1193;  
 Best Local Similarity 34.8%; Pred. No. 5.5e-98;  
 Matches 354; Conservative 177; Mismatches 293; Indels 193; Gaps 33;  
 Qy 65 DFDNSLSLPPAKLVSVFAPSSNEVETTLSDVTLSSLPSNETEKTITIVKTENASG- 123  
 Db 278 dstkisvipgngklll-----gsnqneivslkgdylfnlwnftmakilnslscnvgk 332  
 Qy 124 -----VKPQRNI-----CNLSSTCNDSAFFRGEIMFOY 151  
 Db 333 vvdwqndfwnipnlalkaesnlscgysylipipaaelascadlgticqdgiiyrisvviq- 391  
 Qy 152 DKESTVPQNHITNGTLTGVLSELKRS- LNKTLQTLSETYFTMCATAEAQSTL 206  
 Db 392 -----nlrhpevkqskvaewlnstfgwnyvtvyv-----v 423  
 Qy 207 NCTFTIKLNTMNACAAIAALERVKIRPMEHCCSVRIPCSPSPPEELGKL----- 256  
 Db 424 nlsfhls-----agedkikvk-----rsledeprlwallvyna 458  
 Qy 257 --QCLODQDIVCLADHPRGPPFFSSQSIPIVPRATVLS--QVPKATSAEPDPYSPVTHN 312  
 Db 459 tntnlnlegkili-----qqklklnesldeglrlhtvnrqlghclameepkgy-----y 507  
 Qy 313 VPSPIGEIOP---LSPQPSAPIASSPAIDMPPQSETISSPMPQTHVSGTPPPVKASFSSP 369  
 Db 508 wps-----iqpseyvlpcpdkpgfsasri-----cfynatnplv----- 541  
 Qy 370 TVSAPANVNT--TSAPPVQTDIVNTS-----SISDLENQVLOMEKALSL-GSLEPNLAG 420  
 Db 542 tywgpvdiscnlkeanevanqilntadgqnltsanitniveqvkriynkeeniditlgs 601  
 Qy 421 EMINQVSRLLHSPDMLAPLAQRLKLVVDIGLOLNFNTT- ISLTSPLALAVIRVNAS 479



Db 960 vvlasnnnevgykesygyk---ekgdefcwldqdpvfyvtcagfygvmfllniamfivm 1016  
 QY 831 VOLCRKKKOLGAQRKTSIODLRSIAGLTFLGLTGWGFAFFAWGPNVNTFMFLAIFNT 890  
 Db 1017 vqicgrngksrntlrreenvlrnsvsltflgntwgfaffawgplnlpfmylfsifns 1076  
 QY 891 LQGFIFIFCYCAKENVRKQWRRYLCCGKLRLAENSWSKATNGLKQTVNGVSSSN 950  
 Db 1077 lqglfifhcamkenvgkwrhlcgrfrladnsdsktatkniikssdnlgskslss 1136  
 QY 951 SLOSSS-----NSTNSTTLVNDSCVHAGNGNASTERNGVSEFVQNGDV--CLH 999  
 Db 1137 sigsnstyltsksssttyfkrn-----shdhnvsyeh-----sfn-kgslrqcfh 1183

RESULT 14  
 AAU00210  
 ID AAU00210 standard; Protein; 1221 AA.  
 XX AAU00210;  
 AC AAU00210;  
 DF 12-SEP-2001 (first entry)  
 XX Human novel G-protein coupled receptor, NGPCR#21.  
 DE Human; novel G-protein coupled receptor; NGPCR; antagonist;  
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
 KW abnormal blood pressure; cancer.  
 XX Homo sapiens.  
 OS  
 XX WO200118207-A1.  
 PN 15-MAR-2001.  
 PD 08-SEP-2000; 2000WO-US24591.  
 PF 10-SEP-1999; 99US-0153366.  
 PR 15-NOV-1999; 99US-0165510.  
 XX (LEXI-) LEXICON GENETICS INC.  
 PA Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
 PI Sands AT;  
 XX WPI; 2001-191773/19.  
 DR N-PSDB; AA500130.  
 XX New nucleic acids encoding human G-protein coupled receptors, useful as  
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
 PT disease and cancer -  
 XX Disclosure; Page 118-120; 149pp; English.  
 PS  
 PS The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
 CC The NGPCRs are members of the 7 transmembrane domain class of  
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
 CC them and (ant)agonists of the NGPCRs are useful for the treatment  
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
 CC disease, abnormal blood pressure, cancer and any associated symptoms.  
 CC  
 SQ Sequence 1221 AA;

Query Match 27.0%; Score 1444.5; DB 22; Length 1221;  
 Best Local Similarity 34.6%; Pred. No. 5.7e-98;  
 Matches 350; Conservative 179; Mismatches 295; Indels 187; Gaps 30;

QY 65 DTDNSSLSPPAKLSSVVFAPSSNEVETTSINDVTLSSLPSNETEKTKITIVKTFNASG- 123  
 Db 277 dstiskvipngklll-----gsnqneivskgdiynflwnftmakihslnscnvkgn 331

QY 124 -----VRPQRNI-----CNLSSICNDSAFFGEIMFOY 151  
 Db 332 vvdqndfnipnlalkaesnlscgsyilipaaelaascadgtlclqdgliyrsviq- 390  
 QY 152 DKESTVPQNOHITNGTLTGVLSELSEKSE-----LNKTLQTLSEYFIMCATAEAQSTL 206  
 Db 391 -----nllrhpevkvgkvaewlnstfqwnytvyv-----v 422  
 QY 207 NCTFTIKLNNTMNACAAIAALERKIRPMEHCSCSRIPCPSPPEELGKL----- 256  
 Db 423 nlsfhls-----agedkikvk-----rsledeprlvllwallvyna 457  
 QY 257 --OCDLQDPVLCUADHPRGPPFPSSQSIPVPRATVLS--QVPKATSFABPPDPYPTVHN 312  
 Db 458 tntnlegkii-----qkilkknnesideglrlrltvtvvrqighclameepky-----y 506  
 QY 313 VPSPIGEIQP---LSQPSAPIASSPAIDMPQSETISSPMPQTHVSGTTPPVKASFSSP 369  
 Db 507 wps-----lqpsvylpcdpkpgfsari-----cfynatnplv----- 540  
 QY 370 TVSAPANVNT--TSAPPVQTDIVNTS-----SISDLENQVLQMEKALSL--GSLEPNLAG 420  
 Db 541 tywgpvdinckleanevanqilnltadqnltsanitveqykrivnkeeniditlgs 600  
 QY 421 EMINQVSRLLHSPDMLAPLAQRLLKVVDIGLQNFNWT--ISLTSPLSALAVIRNAS 479  
 Db 601 tlmnifsnllssdsdllessealktidelfakidlnstshvntnrlalsvslpg 660  
 QY 480 SFNTTTFVAODPAN---LOVSLFQAPENSIGTITLPSLMMNLPAHDMELASRVQNF 535  
 Db 661 tnaifnsglpsnnesyfgmdfes-gvqvdplavslpnllelspedsvlvrradftf 719  
 QY 536 FETPALFQDPSLENLSLTSYVSSSVANLTVRNLTRNVTVTLKHINPSQDELAVRCVFW 595  
 Db 720 fnktglfqvgpqrktlsvymacsignitqnlkdpvqikikhttrtqevhhpi-cafwd 778  
 QY 596 LGRNGRGGSNDGCC-SVKDRRLNETICTCSHLTSEGVLLDLST--SVLPAQ--MMALTFFI 652  
 Db 779 lnknsfggwntagcvahrdsdasetvclcnhthfvgvldmiprsasqldarntkvtfi 838  
 QY 653 TYIGCGLSSIFLSVTLVTYIAFEKIRRDYPSKILQOLCAALLNLVFLDLSWTALYKMO 712  
 Db 839 sylgcgisaifsaatlityavafekirrdypskilmlstallfnlflldgwitsfnvd 898  
 QY 713 GLCISAVFLHYFLLVSTWMLGFAFMYLALVKVFNTRYIRKYILKFCIVGWGVAVVVT 772  
 Db 899 glciavavllhffllatftwmgleaahmyialvkfntyirtyllkfcilgwgpalvvs 958  
 QY 773 ILITISPDN--YGLGSYGKFPNGSPDDFCWINNNAVFTYTVGVGFCVIFLLNVSMTIVL 830  
 Db 959 vvlasnnnevgykesygyk---ekgdefcwldqdpvfyvtcagfygvmfllniamfivm 1015  
 QY 831 VOLCRKKKOLGAQRKTSIODLRSIAGLTFLGLTGWGFAFFAWGPNVNTFMFLAIFNT 890  
 Db 1016 vqicgrngksrntlrreenvlrnsvsltflgntwgfaffawgplnlpfmylfsifns 1075  
 QY 891 LQGFIFIFCYCAKENVRKQWRRYLCCGKLRLAENSWSKATNGLKQTVNGVSSSN 950  
 Db 1076 lqglfifhcamkenvgkwrhlcgrfrladnsdsktatkniikssdnlgskslss 1135  
 QY 951 SLOSSS-----NSTNSTTLVNDSCVHAGNGNASTERNGVSEFVQNGD 995  
 Db 1136 sigsnstyltsksssttyfkrn-----shdhsmdksklahadgd 1180

RESULT 15  
 AAU00206  
 ID AAU00206 standard; Protein; 1222 AA.  
 XX AAU00206;  
 AC AAU00206;  
 DF 12-SEP-2001 (first entry)  
 XX

Human novel G-protein coupled receptor, NGPCR#17.  
Human; novel G-protein coupled receptor; NGPCR; antagonist;  
agonist; diabetes; obesity; atherosclerosis; heart disease;  
abnormal blood pressure; cancer.

Homo sapiens.

WO200118207-A1.

15-MAR-2001.

08-SEP-2000; 2000WO-US24591.

10-SEP-1999; 99US-0153366.

15-NOV-1999; 99US-0165510.

(LEXI-) LEXICON GENETICS INC.

Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
Sands AT;

WPI: 2001-191773/19.

N-PSDB; AAS00126.

New nucleic acids encoding human G-protein coupled receptors, useful as  
a therapeutic target for diabetes, obesity, atherosclerosis, heart  
disease and cancer.

Disclosure; Page 105-107; 149pp; English.

The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
The NGPCRs are members of the 7 transmembrane domain class of  
receptors. The NGPCR proteins of the invention, polynucleotides encoding  
them and (ant)agonists of the NGPCRs are useful for the treatment  
of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
disease, abnormal blood pressure, cancer and any associated symptoms.

Sequence 1222 AA;

Query Match 27.0%; Score 1444.5; DB 22; Length 1222;  
Best Local Similarity 34.6%; Pred. No. 5.7e-98;  
Matches 350; Conservative 179; Mismatches 295; Indels 187; Gaps 30;  
QY 65 DTDNSLSPPAKLSVVSFAFSSNEVETSLNDVTLSLPSNETKTIIVKTFNAGS- 123  
DB dtskivpgngklll-----gsnqnelvslkgdiynrlwnftmnaakilsnscvkn 332  
QY 124 -----VKQRNI-----CNLSICNDSAFFRGEIMFOY 151  
DB 333 vvdvgnfdwnipnialkaesnlscgsyilplpaaelascadlgtlqdgilrsvviq- 391  
QY 152 DKESTVPQNHITNGLTGLVLSLKRSE----LNKTLTQTLSETVFIMCATAEASTL 206  
DB 392 -----nilrhpevkqsvaewlnstfgwnyvtvv-----v 423  
QY 207 NCTFTIKLNTMNACAAIALAERVKIRPMEHCCSVRIPCSPSPPEELGKL----- 256  
DB 424 nisfhs-----agedkikvk-----rsledeprlwallvyna 458  
QY 257 --QCQLQDPIVCLADHPGPPSSSQSIDVPVPRATVLS--QVPKATSFAPPDSPVTHN 312  
DB 459 tntnlegkii-----qgkilknesldegirhtvnrqlghclameepkgy-----y 507  
QY 313 VPSPIGEIQP--LSPQPSAPITASSPAIDMPQSEIISPPMPTHVSGTPPVKRAFSSP 369  
DB 508 wps-----lqseyvlpckpgfsasrl-----cfynatnplv----- 541  
QY 370 TVSAPANVNT--TSAPPVQTDIVNTS-----SISLENOVLQMEKALSLS-LSLEPNLAG 420  
DB 542 tywqpvdisnclkeanevanqilnitadgqnitsanitniveqvkriynkeeniditlgs 601

QY 421 EMINQVSRLLHSPDMLAPLAQRLLKVVDDITGLQNFNSNTT-ISLTSPLSALAVIRNAS 479  
DB tlmnifsnlssdsdllessealktidafkidlnstshvnttrlnalsvslpg 661  
QY 480 SPNTTTFVAQDPAN----LQVSLETOAPENSIGTITLPSLLMNNLPAHDMELASRVQFNF 535  
DB tnaifsnfsglpsnnesyfqmdfes-gqvdpilasvilpnlleispedsvlvrqdtf 720  
QY 536 FETPALFQDPSLENLSLISYVISSVANLTVRNLTRNVTVLKHNPSQDELVRVRCVFW 595  
DB fktgldqdvpgqrktivsyvmacsignitqlkdpvqikikhttrtqevhhpi-cafwd 779  
QY 596 LGRNGRGGSWDNGC-SVKDRRLNETICTCSHLTSGVLDDLST-SVLPAQ-MMALTFI 652  
DB lnkksfggwntsgcvahtsdasetvelcnhftghfvmldiprsasqldarntkvtfi 839  
QY 653 TYTGCGLSSTFLSVTLTYIAFEKIRRDYPSKILIQLCALALLNLVFLDLSIALVKMQ 712  
DB sylgcgisalfsaatlityvafekirrdypskilmlstallfinlflldgwitsfnvd 899  
QY 713 GLCISAVFLHYFLVSTWMLGFAFMYLALVKVFENTYIRKYILKPCIVGWGVPVVV 772  
DB glclavavllhffllatftwmgleaahmyialvkvfntyirryilkfciigwglpalvvs 959  
QY 773 IITISPDN--YGLGSGYKFPNGSPDDFCWINNAVFYITVGVFCVIFILNYSMFTVVL 830  
DB vvlasrnnnevygkesygyk---ekgdefcwldqdpvfyfycagfvgmfflinamflv 1016  
QY 831 VOLCRIKKKQLGAQRKTSIODLSRIAGLTFLGTWGAFFAWGPVNVTFMVLFAIFNT 890  
DB vlcgrngksnrtlreevlnlrsvsltilgmltwgfaaffawgplnlpfmylfsfns 1076  
QY 891 LOGFFIFIFYCVAKENVRKQWRRLCCGKRLAENSNDWSTKATNGLKQTVNOGVSSSSN 950  
DB lqglfififihcamkenvgkqwrhlcgfrladsndwsktatniikkssdnigkslss 1136  
QY 951 SLOSSS-----NSTNSTLLVNDCSVHAGNAGNASTERNGVSFVSQNGD 995  
DB sigsnstlytskskssttyfkrn-----shdtsasmkdsisklahadgd 1181

RESULT 16

AAU00715  
ID AAU00715 standard; Protein; 1222 AA.

XX AC AAU00715;

XX DT 12-SEP-2001 (first entry)

XX DE Human novel G-protein coupled receptor, NGPCR#25.

XX KW Human; novel G-protein coupled receptor; NGPCR; antagonist;  
agonist; diabetes; obesity; atherosclerosis; heart disease;  
abnormal blood pressure; cancer.

XX OS Homo sapiens.

XX PN WO200118207-A1.

XX PD 15-MAR-2001.

XX PF 08-SEP-2000; 2000WO-US24591.

XX PR 10-SEP-1999; 99US-0153366.

XX PR 15-NOV-1999; 99US-0165510.

XX PA (LEXI-) LEXICON GENETICS INC.

XX PI Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
Sands AT;

XX DR WPI: 2001-191773/19.

XX DR N-PSDB; AAS00134.

New nucleic acids encoding human G-protein coupled receptors, useful as a therapeutic target for diabetes, obesity, atherosclerosis, heart disease and cancer -

Disclosure; Page 130-133; 149pp; English.

The sequence represents a Human novel G-protein coupled receptor (NGPCR), The NGPCRs are members of the 7 transmembrane domain class of receptors. The NGPCR proteins of the invention, polynucleotides encoding them and (ant)agonists of the NGPCRs are useful for the treatment of diabetes, abnormal body weight or obesity, atherosclerosis, heart disease, abnormal blood pressure, cancer and any associated symptoms.

Sequence 1222 AA;

```

Query Match      27.0%; Score 1444.5; DB 22; Length 1222;
Best Local Similarity 34.6%; Pred. No. 5.7e-98;
Matches 350; Conservative 179; Mismatches 295; Indels 187; Gaps 30;

65 DTDNSLSPPAKLSVVVSFAFSSNEVETSTSDVDTLSLLPSNETEKTKTIIVKTFNASG- 123
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
278 dtsiskvipgngklli-----gsnqneivskgdiynfrlwnftmakllsnlscnvnkg 332
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
124 -----VKPQRI-----CNLSJSDCNDAFFGEIMFQY 151
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
333 vvdgndfwnipnulaikaesnlscgsyilipaaelaascadglgticqdgilyrisvviq- 391
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
152 DKESTVPQNHITNGTILTGVLSELKRSE-----LNKTLQTLSETIYFTMTCATAEAQSTL 206
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
392 -------nllrhpvkvqskvaewlnstfgnwnvtvy-----v 423
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
207 NCTFTIKLNTMNACAAIALERVKIRPMEHCCCSVRIPCSPSPPEELGKL----- 256
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
424 nlshls-----agedkikvk-----rsledeprlviallvyna 458
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
257 ---QCLODPIVCLADHPRGPPFSSQSIPIVVPRAIVLS--QVPKATSAFEPDPYSPVTHN 312
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
459 tntnlegklli-----gqkllknesldeglrlhtvnrqlghclameepkgy-----y 507
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
313 VPSPIGEIOP--LSPQSPAPIASSPAIDMPPQSETISSPMPQTHVSGPFPVVKASFSSP 369
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
508 wps---lqpsyylvpcdkpgfsari-----cfynatnply----- 541
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
370 TVSAPANVNT--TSAPPVQNDIVNTS-----SISDLENQVLMQEKALS-GLSEPNLAG 420
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
542 tywgvpdisclikeanevanqilnltadgqnltsanitniveqvrkrivkeeniidtlgs 601
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
421 EMINQVSRLLHSPDDMLAPLQORLLKVVDDIGLQNFNTT-ISTSPSLALAVIRVNAS 479
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
602 tlmnlfnlssdsdlseesaelktidelafkldinstshvnltnrlalsvsilpg 661
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
480 SFNTFTTFAQDPAN----LQVLSLETQAPENSIGITLPSLLMNNLPAHDMELASRVQFNF 535
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
662 tnaiafnsglspnnesyfqmdfes-gqvdpasvillppnllenlspedsvllvrraqftf 720
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
536 FETPALFQDPSLENLSLSVYVSSSVANLTVRNLTRNVYTLKHINPQODELTVRGVFWD 595
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
721 fnktglfgvgqrktlvsyvmacsignitqnlkdpvgikikikrtqdevghpi-cafd 779
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
596 LGRNGRGGWSNGC-SVKDRRLRNETICTSHLTSFGVLLDLSRT-SVLPAAQ-MMALRTI 652
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
780 lnknksfgwntsgcvahrdsasetvclcnhfhfgyvldmplrasagldarntkvlftfi 839
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
653 TYIGCGLSSIFLVSUVTLVYIAFEKIRRDYPSKILQICAAALLLNVLFLSWIALYKMK 712
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
840 syvgcisaifaatltyvafeklrrdypskilmnltallnllfldgwitsfnvd 899
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
713 GLCISVAVFLHVLVSVFMGLEAFHMLALVKVFNTYIRKYTLKFCIVGCVFNAVVT 772
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
900 glclavavllhflfatfcmwgleahmyialvkvfntyrriakfcilgwiglpalvys 959
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

Qy	773	ILITSPDN--YGLGSYGKFPNGSPDDFCWNNNAVFYITVVGVCYFVIFLLNVSMFIVVL	830
		: :     :           :         :           :     :     :         :	
Db	960	vvlaarnnnevgykesyk--ekgdefcwqdpvifvvtcagyfygmfflniamfivm	1016
Qy	831	VOLGRKKKKQLGQAOKTSTIQDLRSIAGLTFLLGITWGEFAFFAWGPNVTFMYLFAFNT	890
		:     :   : :       :         :                     :             :	
Db	1017	vqicgrngkrnsrtlrreevlnlrsvsiltflgmtwgfaffawgplnlpfmylfsifns	1076
Qy	891	LQGFPIFFTCYCAKENVSKQWPRYLCCKGLRLAENSDWSKTATNGLKKOTVQGVSSSSN	950
		:   :	
Db	1077	lqglfifliffhamenvqkwrhlccgrfrladsdwsktatnlkksdnlgkslss	1136
Qy	951	SLOSSS-----NKTNSTTLLVNNDCSVHAGSNGNASTERNCGVSFVQNGD	995
		:   :   : :         :                 :     :   : : :     :	
Db	1137	signstnyltkskssttyfkn-----shtdsasmksklahadgd	1181
RESULT	17		
ID	AAU00203		
AAU00203	standard; Protein; 512 AA.		
AC	AAU00203;		
XX			
XX			
DT	12-SEP-2001 (first entry)		
XX			
DE	Human novel G-protein coupled receptor, NGPCR#14.		
XX			
KW	Human; novel G-protein coupled receptor; NGPCR; antagonist;		
KW	agonist; diabetes; obesity; atherosclerosis; heart disease;		
KW	abnormal blood pressure; cancer.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200118207-AL.		
XX			
PD	15-MAR-2001.		
XX			
PF	08-SEP-2000; 2000WO-US24591.		
XX			
PR	10-SEP-1999; 99US-0153366.		
PR	15-NOV-1999; 99US-0165510.		
XX			
PA	(LEXI-) LEXICON GENETICS INC.		
XX			
PI	Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;		
PI	Sands AT;		
XX			
PI	WPI; 2001-191773/19.		
DR	N-PSDB; AAS00123.		
DR			
PT	New nucleic acids encoding human G-protein coupled receptors, useful as		
PT	a therapeutic target for diabetes, obesity, atherosclerosis, heart		
PT	disease and cancer -		
XX			
PS	Disclosure; Page 101-102; 149pp; English.		
XX			
CC	The sequence represents a Human novel G-protein coupled receptor (NGPCR)		
CC	The NGPCRs are members of the 7 transmembrane domain class of		
CC	receptors. The NGPCR proteins of the invention, polynucleotides encoding		
CC	them and (ant)agonists of the NGPCRs are useful for the treatment		
CC	of diabetes, abnormal body weight or obesity, atherosclerosis, heart		
CC	disease, abnormal blood pressure, cancer and any associated symptoms.		
XX			
SQ	Sequence 512 AA;		
SQ			

```

Query Match.          25.6%; Score 1372.5; DB 22; Length 512;
Best Local Similarity 52.6%; Pred. No. 3.6e-93;
Matches 266; Conservative 89; Mismatches 124; Indels 27; Gaps 11;

OY 507 IGTTLPSLMNNLPAHDMELASRQVQNFETPTALFQDPSSLNLSIYSVISSVANLTV 566
db 11 lasvllppllenlpedsavlvragftfnktglfqdvqpqrklvsvmacsqnlti 70

```



12-SEP-2001 (first entry)  
Human novel G-protein coupled receptor, NGPCR#13.  
Human; novel G-protein coupled receptor; NGPCR; antagonist;  
agonist; diabetes; obesity; atherosclerosis; heart disease;  
abnormal blood pressure; cancer.  
Homo sapiens.  
WO200118207-A1.  
15-MAR-2001.  
08-SEP-2000; 2000WO-US24591.  
10-SEP-1999; 99US-0153366.  
15-NOV-1999; 99US-0165510.  
(LEXI-) LEXICON GENETICS INC.  
Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
Sands AT;  
WPI; 2001-191773/19.  
N-PSDB; AAS00122.  
New nucleic acids encoding human G-protein coupled receptors, useful as  
a therapeutic target for diabetes, obesity, atherosclerosis, heart  
disease and cancer -  
Disclosure; Page 99-100; 149pp; English.  
The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
The NGPCRs are members of the 7 transmembrane domain class of  
receptors. The NGPCR proteins of the invention, polynucleotides encoding  
them and (ant)agonists of the NGPCRs are useful for the treatment  
of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
disease, abnormal blood pressure, cancer and any associated symptoms.  
Sequence 541 AA;  
Query Match 25.6%; Score 1372.5; DB 22; Length 541;  
Best Local Similarity 52.4%; Pred. No. 3.9e-93;  
Matches 262; Conservative 91; Mismatches 126; Indels 21; Gaps 8;  
QY 507 IGTITLPSLLMNLPAHDMELASRVQNFETPALFQDPSLENLSISVIVSSVANLTV 566  
Db 11 lasvilpnllelspedavlvrraqftffnkgtlfgdvgpqrktlvsvymacsigniti 70  
QY 567 RNLTRNVTLKHINPSQDELATVRCVFDLGRNGRGWSNCG-SVKDRRLNETICTCS 625  
Db 71 qnlkdpvqikikhtreqevhpi-cafdlnknksfgwntsgcvahrdsdasetvclcn 129  
QY 626 HLTSGVLLDLST-SVLPAPQ-MMALTFIYICGLSIFILSVILVTYIAEKIRRDYPS 583  
Db 130 hfthfgvmdlpisaslqdarntkvtifsiyigcgsaifsaatlityvafeklrldyps 189  
QY 684 KILIQCAALLNLLVFLDLSDIALYKMOGLCISVAVFLHYFLVFLVFTWMLGFAFHYLA 743  
Db 190 kilmalstallfnllldgwtstfnvdlciavavllhffllatftwglmleahmyia 249  
QY 744 LVKVENTYRKILFCIVGWGPAVVVITLISPDN-YGLSGSYGFPNGSPDFDCWI 801  
Db 250 lkvfntyirryllkciigwgpilavsvvlasmnnevgykesygk---ekgdefcwi 306  
QY 802 NNAVYITVWGYFVIFLNLVSMFIVLVQLGRIKKKQLGAKRKTSIQDLRSTAGLTF 861  
Db 307 qdpvifvtcaegfygmfflamflvmvqicgrngdkrsnrtlreevrlrlsvsvstf 366  
QY 862 LLGTWGAFFAWGPVNVTFMYLFAIFNTLQGFIFIFYCVAKENVRKQWRYLCCGKLRL 921

Db 367 llgmtwgfaffawgplnlpfmylfsifnslgqlffifhcamkenvgkwrhrhccgrfr 426  
QY 922 LAENDWSKTATNGLKKQTVNQGVSSSSNSLQSSS-----NSTNSTTLLVNNDCSVHAS 975  
Db 427 ladnsdwsktatnlikksdnlksslsnsgnstylytsksssttyfkrn-----s 480  
QY 976 GNGNASTERNQVSPFVQNGD 995  
Db 481 htcdasmkdsksklahadgd 500  
RESULT 20  
AAU00197  
ID AAU00197 standard; Protein; 1111 AA.  
XX  
AC AAU00197;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human novel G-protein coupled receptor, NGPCR#8.  
XX  
KW Human; novel G-protein coupled receptor; NGPCR; antagonist;  
KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
KW abnormal blood pressure; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200118207-A1.  
XX  
PD 15-MAR-2001.  
XX  
PF 08-SEP-2000; 2000WO-US24591.  
XX  
PR 10-SEP-1999; 99US-0153366.  
PR 15-NOV-1999; 99US-0165510.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;  
PI Sands AT;  
XX  
DR WPI; 2001-191773/19.  
DR N-PSDB; AAS00117.  
XX  
PT New nucleic acids encoding human G-protein coupled receptors, useful as  
PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
PT disease and cancer -  
XX  
PS Disclosure; Page 84-86; 149pp; English.  
XX  
CC The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
CC The NGPCRs are members of the 7 transmembrane domain class of  
CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
CC them and (ant)agonists of the NGPCRs are useful for the treatment  
CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart  
CC disease, abnormal blood pressure, cancer and any associated symptoms.  
XX  
SQ Sequence 1111 AA;  
Query Match 22.5%; Score 1205; DB 22; Length 1111;  
Best Local Similarity 33.8%; Pred. No. 2.8e-80;  
Matches 310; Conservative 166; Mismatches 306; Indels 136; Gaps 30;  
QY 68 NSSLPPPAKLWSVSPAPSNE---VETTSINDVTLSPNEETKTKITIVKTFNASCV 124  
Db 233 mnal---pvkedifaeefqclvwnslsgsvnfkrnyetvpcdstsk-----v 283  
QY 125 KPQRNICLSSICNDSAPFRGEIMFYQDKESTVPQNOHITNGTLTGLVLSLSEKRSLELNK 184  
Db 284 ipgngklllgsnqnqlsvlskqdi-----ynfrlwnftmnaki-lslslscnvkgn 331

PN	WO200118207-A1.	
XX		
PD	15-MAR-2001.	
XX		
PF	08-SEP-2000; 2000WO-US24591.	
XX		
PR	10-SEP-1999; 99US-0153366.	
PR	15-NOV-1999; 99US-0165510.	
XX		
PA	(LEXI-) LEXICON GENETICS INC.	
XX		
PI	Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;	
PI	Sands AT;	
DR	WPI; 2001-191773/19.	
DR	N-PSDB; AAS00113.	
XX		
XX	New nucleic acids encoding human G-protein coupled receptors, useful as	
PT	a therapeutic target for diabetes, obesity, atherosclerosis, heart	
PT	disease and cancer -	
PS	Disclosure; Page 71-73; 149pp; English.	
XX		
XX	The sequence represents a Human novel G-protein coupled receptor (NGPCR).	
CC	The NGPCRs are members of the 7 transmembrane domain class of	
CC	receptors. The NGPCR proteins of the invention, polynucleotides encoding	
CC	them and (ant)agonists of the NGPCRs are useful for the treatment	
CC	of diabetes, abnormal body weight or obesity, atherosclerosis, heart	
CC	disease, abnormal blood pressure, cancer and any associated symptoms.	
XX		
XX	Sequence 1112 AA;	
QY	Query Match 22.5%; Score 1205; DB 22; Length 1112;	
Db	Best Local Similarity 33.8%; Pred. No. 2.8e-80;	
XX	Matches 310; Conservative 166; Mismatches 306; Indels 136; Gaps 30;	
QY	68 NSSLPPPPAKLSVVSFAPSNE---VETTSINDVTLTSLSPNEETKTIIVKTFNAGSV 124	
Db	234 nnaal---pykekedifaesfeqiclvwnnsgisgvnfkrnyetvpcdstisk-----v 284	
QY	125 KPORNICNLSSINDSAFFRGEIMFOYDKESTVPQNHITNGTLTGLVLSSELKRSLELNK 184	
Db	285 ipngngklllgnsqneivslkgdl-----ynfrlwnftmnaki-lsnlscnvkgn 332	
QY	185 TLQTLSETYFMCAATAEAQSTLNC-TFTIKLNNT-MNACAAIAALERVKIRPMEHCCSV 242	
Db	333 vvdwqndfwnlpnlalkaesnlscgsylipaaelascadlgtl-----cqatv 382	
QY	243 RIPCPSSPEELGKLCQDLQDPVCLADHPR--GPPFSSS---QSIPVVPVPRATVLSQVPK- 296	
Db	383 nspsttpvttnm-----pvtndrkqndglliyrisvviqnlrhpekvqskvae 436	
QY	297 ATSAEPDPDYSPVTHNV-----PSPIGEIQPLSPQP-----	327
Db	437 lnstfgwnyvyvvnifshlsagedkikvkrsldeprlvllwallvynatntnlegki 496	
QY	328 --SAPIASSPAIDMPPQSETIS-----SPMPQTHVSGTTPPVKASF 366	
Db	497 iqqklklnnesldegrlhtvnrqlghclameepkgyvwpisqpsyv--lpcpdkpgf 554	
QY	367 S-----SPTVS--APANVNT--TSAPPVQTDIVNTS-----SISDLENQVLOME 406	
Db	555 sasricfynatnplvtygvpvdisncikneanvanqilnltadggnltsanitniveqvk 614	
QY	407 KALS-LSLENLAGEINQVSRLLHSPDMLAPLAORLLKVVDDIGLQNFSTNT-LSL 464	
Db	615 rivnkeeniiditlgtlmnifsnlssdsdillessealktldelafkidlnstshvni 674	
QY	465 TSPSLALAVIRVNASSFNTTFFVAQDPAN---LQVSLQAPENSIGTITLPSLMMNL 520	
Db	675 trnlalsvslpntnaisnfsiglpnsnesyfqmdfes-gqvdpilasvilppnllenl 733	

Qy 521 PAHDMELASRVQNFETPALFQDPSPLENLSLISVSISSVANLTVRNLTNRVTVTLKHI 580  
 Db 734 spedsvlvrraqftfnktglfqdvpgqrktlvsvymacsignitqnlkdpvqikikt 793  
 Qy 581 NPSQDELTVRCVFDLGRNGRGWSNCGC-SVKDRRLNETICTCSHLTSFGVLLDLST 639  
 Db 794 rtqevhhpi-cafwltnkksfggwntsgcvahrdsdasetvclcnhftfghvldmldpr 852  
 Qy 640 -SVLPAQ-MMALTFITVIGCGLSIFLSVTLVTVIAPEKIRRDYPSKILTOICAAALLLN 697  
 Db 853 asqldarntkvlfsiygogisafsaatlityvafekirrdydpksklmnlstallfn 912  
 Qy 698 LVFLDLSWIALYKMOGLCISVAVFLHYFLVLSFTWMGLEAFHMYLALVKVFNTYIRKYL 757  
 Db 913 lllfldgwitsfnvdlciavavllhffllatftwmgleaahmyialkvfntyirryil 972  
 Qy 758 KFCIVGWGPVAVVVVITILTISPDN--YGLSGYKFPNGSPDDFCWINNAVFIYTVVG 815  
 Db 973 kfciigwglpalvsvvlasrnnnevgykesygk---ekgdefcwldqpvifvvtcagf 1029  
 Qy 816 CVIFLLNVMFIVVLVQLCRICKKKQLGAQRKTSIQDLRSIAGLTFLGIGTWGFAFFAW 875  
 Db 1030 gvmfflniamfivvmvqicgrngkrnsrtlrreelnrlsvvslftlglmtwgfafaw 1089  
 Qy 876 PNVNVTMYLFAFNTLOG 893  
 Db 1090 plnlpmylfsifnslgq 1107

## RESULT 22

AAU00201  
 ID AAU00201 standard; Protein; 1112 AA.

AC AAU00201;

DT 12-SEP-2001 (first entry)

DE Human novel G-protein coupled receptor, NGPCR#12.

KW Human; novel G-protein coupled receptor; NGPCR; antagonist;  
 KW agonist; diabetes; obesity; atherosclerosis; heart disease;  
 KW abnormal blood pressure; cancer.

OS Homo sapiens.

PN WO200118207-A1.

XX 15-MAR-2001.

PF 08-SEP-2000; 2000WO-US24591.

PR 10-SEP-1999; 99US-0153366.

PR 15-NOV-1999; 99US-0165510.

XX (LEXI-) LEXICON GENETICS INC.

PA Turner CA, Nehls M, Friedrich G, Scoville J, Zambrowicz B;

PI Sands AT;

DR WPI; 2001-191773/19.

DR N-PSDB; AAS00121.

PT New nucleic acids encoding human G-protein coupled receptors, useful as  
 PT a therapeutic target for diabetes, obesity, atherosclerosis, heart  
 PT disease and cancer -

XX Disclosure; Page 96-99; 149pp; English.

XX The sequence represents a Human novel G-protein coupled receptor (NGPCR).  
 CC The NGPCRs are members of the 7 transmembrane domain class of  
 CC receptors. The NGPCR proteins of the invention, polynucleotides encoding  
 CC them and (ant)agonists of the NGPCRs are useful for the treatment  
 CC of diabetes, abnormal body weight or obesity, atherosclerosis, heart

CC disease, abnormal blood pressure, cancer and any associated symptoms.  
 XX  
 SQ Sequence 1112 AA;

Query Match 22.5%; Score 1205; DB 22; Length 1112;  
 Best Local Similarity 33.8%; Pred. No. 2.8e-80;  
 Matches 310; Conservative 166; Mismatches 306; Indels 136; Gaps 30;

Qy 68 NSLSLPPPAKLSSVVSFAPSSENE---VETTSINDVTLVSLSPNETEKTITIVKTFNASGV 124  
 Db 234 nnal---pvkekedifaesfeqlclvwnnslgsigvfnkrnyetvpcdstisk-----v 284  
 Qy 125 KPQRNICNLISSICNDSAFFRGEIMFOYDKESTVPOHQHITNGTLGVLSLSELKRSLELNK 184  
 Db 285 ipngngklllgsgnqneivslkgdi-----ynfrlwnftmaki-lsnlscnvkgn 332  
 Qy 185 TIQTUSETVFIMCATABAQATLNC-TFTIKLNN-TMNAACAIAALERVKIRPMEHCSCSV 242  
 Db 333 vvdwqndfnipnalakaesnlscgyliplaaelascadlgtl-----cgatv 382  
 Qy 243 RIPCPSSPEELGKLQCDLQDPIVCLADHPR--GPPFSSS---QSIPVVPRATVLSQVPK- 296  
 Db 383 nspsttpptvttnm-----pvtmrldqndgiilrvisvignlrlhrhpevkvgkvaew 436  
 Qy 297 ATSFAPPPDYSPVTHNV-----PSPICEIQPLSPQP-----SISDLNQLVOME 327  
 Db 437 lnstfgwnytyvvnisfhlsagedkikvksrledeprlvllwallvynatnntnlegki 496  
 Qy 328 --SAPTASSPAIDMPPQSETIS-----SPMPTHVSGTTPPVKASF 366  
 Db 497 igqkllknnesldeglrlhtvnrqlghclameepkgyvwpisqpsyev--lpcpdkpgf 554  
 Qy 367 S-----SPTVS--APANVT--TSAPPVQDIDVNTS-----SISDLNQLVOME 406  
 Db 555 saaricfynatnplvtyvgpvdinsckieanevanqilnltadgqnltsanitniveqvk 614  
 Qy 407 KALSL-GSLEPNLAGEMINOVSRLLHSPDMLAPIAQLRLKVVDDIGLOLNFSTT-ISL 464  
 Db 615 rivnkeeniditlgstlmnifsnlssdsdlsesseaalktidelafklidlnstshvni 674  
 Qy 465 TSPSLALAVIRVNASSENTTFVAQDPAN---LQVLETAQAPENSIGITITLPSLNNL 520  
 Db 675 trnlalsvslipgtnaaisnfsiglpnsesyfmdfes-ggvdpilasvllppnllenl 733  
 Qy 521 PAHDMELASRVQNFETPALFQDPSPLENLSLISVSISSVANLTVRNLTNRVTVTLKHI 580  
 Db 734 spedsvlvrraqftfnktglfqdvpgqrktlvsvymacsignitqnlkdpvqikikt 793  
 Qy 581 NPSQDELTVRCVFDLGRNGRGWSNCGC-SVKDRRLNETICTCSHLTSFGVLLDLST 639  
 Db 794 rtqevhhpi-cafwltnkksfggwntsgcvahrdsdasetvclcnhftfghvldmldpr 852  
 Qy 640 -SVLPAQ-MMALTFITVIGCGLSIFLSVTLVTVIAPEKIRRDYPSKILTOICAAALLLN 697  
 Db 853 asqldarntkvlfsiygogisafsaatlityvafekirrdydpksklmnlstallfn 912  
 Qy 698 LVFLDLSWIALYKMOGLCISVAVFLHYFLVLSFTWMGLEAFHMYLALVKVFNTYIRKYL 757  
 Db 913 lllfldgwitsfnvdlciavavllhffllatftwmgleaahmyialkvfntyirryil 972  
 Qy 758 KFCIVGWGPVAVVVVITILTISPDN--YGLSGYKFPNGSPDDFCWINNAVFIYTVVG 815  
 Db 973 kfciigwglpalvsvvlasrnnnevgykesygk---ekgdefcwldqpvifvvtcagf 1029  
 Qy 816 CVIFLLNVMFIVVLVQLCRICKKKQLGAQRKTSIQDLRSIAGLTFLGIGTWGFAFFAW 875  
 Db 1030 gvmfflniamfivvmvqicgrngkrnsrtlrreelnrlsvvslftlglmtwgfafaw 1089  
 Qy 876 PNVNVTMYLFAFNTLOG 893  
 Db 1090 plnlpmylfsifnslgq 1107



Db 143 LNTQTLWRTGREGISSTAFITILRDVESKVLKTDPE-----QKVLKIQND----- 190  
 QY 457 FSNNTISLSPSLALAVIRVNASSFNTEVAQDPANLOYSL-----ETQAP 503  
 Db 191 -----SVALETQAITDNCSEERKT-----FNLVQNMNSMDIRCSIIQDGTQGP 234  
 QY 504 ENSIGTITLPSLMMNLPAHDMELASRVQNFETPALFQDPSLENLSIVYSSSVAN 563  
 Db 235 -SAIAFISYSS-----LGNIIATFFE-----EMDKKDQVYLSQVVSAAIGP 276  
 QY 564 LTVRNLTNRVTVTLKHINPSODELTVRCVFDWDLGRNGRGG--WSDNGCQSVKDRRLNETIC 622  
 Db 277 KRNVSLSKSVTLTFQHVKMTPTSKKVCVYW---KSTQGSQWSRDGCFLIHWNKSHTM 333  
 QY 623 TCSHLTSFGVLDLSDTSVLPQMMALTFITYICGGLSSIFLSVTLVTVYIAFEKIRRDYP 682  
 Db 334 NCSSLSSFAVLMALTSQEDP---VLTVTYVGLSVSLCLLLAALTEFLCKAIONTST 389  
 QY 683 SKILIOCAALLLNVLFLDLSWIALYKMQGLCISVAVFLHYFLVSVFTWMLGFAHMYL 742  
 Db 390 S-LHLQLSLCLFLAHLFLVVG--IDRTEPKVLCSTIAGALHYLYLAFTWMLLEGVHFL 446  
 QY 743 AL--VKVFNTYIRKYILKFCI--VGVGVPVAVVTVIILITISPDNYGLSGYKFPNGSPDDF 798  
 Db 447 TARNLTVVNYSSINRLMKWIMFPGVGYGPAVTVVAISAASWPHLYGTA-----DR 495  
 QY 799 CWINNNAVFTYTVGVFCVIFLLNVSMFIVLVOLCRKKKKQKGAORKTSTIODLRSIA- 857  
 Db 496 CWLHLDQGFMSFELGPVCAIFSANLVFLVFWILKR--KLSSLNSEVST-IQNTMLAF 552  
 QY 858 ---GLTFLGITWGFAPFANGPVNVTEMYLEAFNTLQGFIFIFCYCAKENVRKQWRY 914  
 Db 553 KATAQLFILGCTWCLGLLQVGPAAQVMAYLFTIINSLOGFFIFLVYCLLSQOVQKQYQKW 612

## RESULT 3

US-09-110-116-1  
 ; Sequence 1, Application US/09110116  
 ; Patent No. 6013479  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Hong  
 ; APPLICANT: Cohan, Victoria L.  
 ; APPLICANT: Stuart, Susan G.  
 ; TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN COUPLED  
 ; FILE REFERENCE: PF-0550 US  
 ; CURRENT APPLICATION NUMBER: US/09/110,116  
 ; CURRENT FILING DATE: 1998-07-02  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 652  
 ; TYPE: PRT  
 ; ORGANISM: HOMO SAPIENS  
 ; FEATURE:  
 ; OTHER INFORMATION: 429905, EOSINOT03  
 US-09-110-116-1

Query Match 9.48; Score 500.5; DB 3; Length 652;  
 Best Local Similarity 29.1%; Pred. No. 9.2e-32;  
 Matches 157; Conservative 92; Mismatches 198; Indels 93; Gaps 19;

QY 398 LENOVL-OMEKALSLGSLPDLNAGEMINOVSRLLHSPDMLAPLQRLKVVDDIGLQLN 456  
 Db 143 LNTQTLWRTGREGISSTAFITILRDVESKVLKTDPE-----QKVLKIQND----- 190  
 QY 457 FSNNTISLSPSLALAVIRVNASSFNTEVAQDPANLOYSL-----ETQAP 503  
 Db 191 -----SVALETQAITDNCSEERKT-----FNLVQNMNSMDIRCSIIQDGTQGP 234  
 QY 504 ENSIGTITLPSLMMNLPAHDMELASRVQNFETPALFQDPSLENLSIVYSSSVAN 563

Db 235 --SVIAFISYSSLGNIIINA-----TFFE-----EMDKKDQVYLSQVVSAAIGP 276  
 QY 564 LTVRNLTNRVTVTLKHINPSODELTVRCVFDWDLGRNGRGG--WSDNGCQSVKDRRLNETIC 622  
 Db 277 KRNVSLSKSVTLTFQHVKMTPTSKKVCVYW---KSTQGSQWSRDGCFLIHWNKSHTM 333  
 QY 623 TCSHLTSFGVLDLSDTSVLPQMMALTFITYICGGLSSIFLSVTLVTVYIAFEKIRRDYP 682  
 Db 334 NCSSLSSFAVLMALTSQEDP---VLTVTYVGLSVSLCLLLAALTEFLCKAIONTST 389  
 QY 683 SKILIOCAALLLNVLFLDLSWIALYKMQGLCISVAVFLHYFLVSVFTWMLGFAHMYL 742  
 Db 390 S-LHLQLSLCLFLAHLFLVVG--IDRTEPKVLCSTIAGALHYLYLAFTWMLLEGVHFL 446  
 QY 743 AL--VKVFNTYIRKYILKFCI--VGVGVPVAVVTVIILITISPDNYGLSGYKFPNGSPDDF 798  
 Db 447 TARNLTVVNYSSINRLMKWIMFPGVGYGPAVTVVAISAASWPHLYGTA-----DR 495  
 QY 799 CWINNNAVFTYTVGVFCVIFLLNVSMFIVLVOLCRKKKKQKGAORKTSTIODLRSIA- 857  
 Db 496 CWLHLDQGFMSFELGPVCAIFSANLVFLVFWILKR--KLSSLNSEVST-IQNTMLAF 552  
 QY 858 ---GLTFLGITWGFAPFANGPVNVTEMYLEAFNTLQGFIFIFCYCAKENVRKQWRY 914  
 Db 553 KATAQLFILGCTWCLGLLQVGPAAQVMAYLFTIINSLOGFFIFLVYCLLSQOVQKQYQKW 612

## RESULT 4

US-09-110-116-4  
 ; Sequence 4, Application US/09110116  
 ; Patent No. 6013479  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Hong  
 ; APPLICANT: Cohan, Victoria L.  
 ; APPLICANT: Stuart, Susan G.  
 ; TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN COUPLED  
 ; FILE REFERENCE: PF-0550 US  
 ; CURRENT APPLICATION NUMBER: US/09/110,116  
 ; CURRENT FILING DATE: 1998-07-02  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 344  
 ; TYPE: PRT  
 ; ORGANISM: HOMO SAPIENS  
 ; FEATURE:  
 ; OTHER INFORMATION: 29355597, GenBank  
 US-09-110-116-4

Query Match 8.7%; Score 463; DB 3; Length 344;  
 Best Local Similarity 33.5%; Pred. No. 3.4e-29;  
 Matches 130; Conservative 59; Mismatches 145; Indels 54; Gaps 15;

QY 589 VRCVFDWDLGRNGRGGWSDNGCQSVKDRRLNETICTCSHLTSFGVLL---DLRSSTVLPQAQ 645  
 Db 2 VLVCFWEHQGN--GCGHWATGCGSTIGTRDTSTICRCHLSSFAVLMAYHVDQEDPV---- 56  
 QY 646 MMALTFITYICGGLSSIFLSVTLVTVYIAFEKIRRDYPVKSLIOLCAALLLNVLFLDLSW 705  
 Db 57 ---LTVITYMGLSVSLCLLLAALTEFLCKAIONTSTS-LHLQLSLCLFLAHLFLVAID 112  
 QY 706 IALYKMQGLCISVAVFLHYFLVSVFTWMLGFAHMYLA---LVKVFNTYIRKYILKFCI- 761  
 Db 113 QTGHKV--LCSIAGTLHYLYLATFTWMLLEALYLFETARNLTWVNYSSINREMKLMFP 170  
 QY 762 VGVGVPVAVVTVIILITISPDNYGLSGYKFPNGSPDDFCWINNNNAVFTYVVGFCVIFLL 821  
 Db 171 VGVGVPVAVVTVIILITISPDNYGLSGYKFPNGSPDDFCWINNNNAVFTYVVGFCVIFLL 821  
 QY 822 NVSMFIVVL-VOLCRKKK-KKOLGAORKTSTIODLRSIAGTLTEFLGLTWGFAFFAWGPVNV 879

Db 220 NLVFLVLTWILKNRLLSSNSEVSTLRNTRMLAFKATAQL-FILGCTWCLGILQVGPAA 278  
QY 880 TFMFLFAFNTLQGFIFIFCYVAKENVRKWRRLCCGKRLAENSDWSKTATNGLKKQ 939  
Db 279 VMAYLFTIINSLQGVFLVYCLLSQVREQY-----GK-----WSK-----GIRKL 320  
QY 940 TVNQGVSNSNSLQSSNSNTSTLLVN 967  
Db 321 K-----TESEMHTLSSAKADTSKPSTVN 344

Db 435 IESKVINKEC-----SEENVTLDLVAKGDKMKIGCSTIEES--ESTETTGVAFVSFVGME 488  
QY 536 FETPALPOD-----PSLENLSLSYVISSSVANLTVRNLTNRNVTTLKHINPSQDELTV 589  
Db 489 VLNERFQDHOAPLTTSEIKLKMSRVVGGIWTGKKGDFSDPIIYTLLENVQPKQKFERP 548  
QY 590 RCVFWDLGRNGRGSGSDNGSVKDRRLNETICTSHLTSFGVLLDLSTSVLPAAOMMAL 649  
Db 549 ICYSWSSTDVKGGR--WTSFGCVILEASETYTSCNQANLAVIMASGELTM-----DFSL 602  
QY 650 TPTYICGSLSSIFLSVTLVYIAFEKTRRDYPSKILLTOLCAALLLNVLVLLDLSWIALY 709  
Db 603 YIISHVGIIISLVLCLVLAIAITFLCRSI--RNHTYTLHLHLCLVCLLAKTLEL-----AGIH 657  
QY 710 KMOGL--CISVAVFLHVFLVFTWMLGFAFMYLAL--VKVFNTYIRKYI--LKFCIVG 763  
Db 658 KDNKTCGAIITAGFLHYFLACFFWMLVEAVILFLVMRLKVVNYFSSRNKMLHICAFG 717  
QY 764 WGPVAVVVTIITISPDNYGLSGYKFPNGSPDDFCWNNNAVFIYTVVGYFCVIFLLNV 823  
Db 718 YGLPMLVVVISASVOPQGYM-----HNRCLNTETGFIWSFLGVPCTVIVIN- 765  
QY 824 SMFIVLVOLCRKKK--QLGAQRKTSIQDLRSTAGLTFLGITWGAFFAWGPNVNT 880  
Db 766 SLLTWTLLRQLSSVNAEVSTLTKLTLTKFAQL-FILGCSWVLGIFQIGPVAGV 824  
QY 881 FMYLFAIFNTLQGFIFIFCYVAKENVRKWRRLCCGKRLAENSDWSK 930  
Db 825 MAYLFTIINSLQGAFLIHLCLLNGQVREYKRWI--TGTKPSSQSQTSR 873

RESULT 6  
US-08-852-806-2  
; Sequence 2, Application US/08852806  
; Patent No. 5874245  
; GENERAL INFORMATION:  
; APPLICANT: Shoji Fukusumi  
; APPLICANT: Shuji Hinuma  
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/852,806  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/017,915  
; FILING DATE: 16 MAY 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: TAK50002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1052 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

Db 220 NLVFLVLTWILKNRLLSSNSEVSTLRNTRMLAFKATAQL-FILGCTWCLGILQVGPAA 278  
QY 880 TFMFLFAFNTLQGFIFIFCYVAKENVRKWRRLCCGKRLAENSDWSKTATNGLKKQ 939  
Db 279 VMAYLFTIINSLQGVFLVYCLLSQVREQY-----GK-----WSK-----GIRKL 320  
QY 940 TVNQGVSNSNSLQSSNSNTSTLLVN 967  
Db 321 K-----TESEMHTLSSAKADTSKPSTVN 344

Query Match 8.2%; Score 438; DB 3; Length 886;  
Best Local Similarity 20.8%; Pred. No. 1.6e-26;  
Matches 198; Conservative 149; Mismatches 365; Indels 238; Gaps 38;

QY 64 EDTNSSLSPPPA-----KLSVVS--FAPSSNE-----VEITSLND-VT 99  
Db 79 KDIDECOSPOCPGPNSSCKNLGRYKSCIDGFSPTGNDWVPGKPGNFSCDINECLT 138  
QY 100 LSLPLSNTEKTIIVKTFNAGVYKPNQICNLSSICNDLSAFFRGEIMFQYDKESTVPO 159  
Db 139 SRVCPHS-----DCVNSMGSYSCSQGVGFISSNSTCEDV-----NECADPR 180  
QY 160 --NOHIT-NGTL-----TGVLSELKRS-----ELNKTLOTLS 191  
Db 181 ACPEHATCNVTGNYSCFNFGEFSSGHLSCQGLKASCEDIDECEMCPINSTCTNTPG 240  
QY 192 TYFTMCATAEAQSTLNCFTIKLNTMNACAAALERVKIRPMEHC-----CCSVRIPC 246  
Db 241 SYFTCHPGFAPSSGQLNFTD-----QVCECRDIDECRODPSTCGPNSIC 285  
QY 247 PSSPEELGKLCQDLQDPITVCLADHPGPP-----FSSQSI-----PVPVRAVLSQVKA 297  
Db 286 TNA---LGSYSCG---IVGFHPNPEGQKGNFSCQVLFKCKEDVDPNKKIQOQCEG 339  
QY 298 TSFAEPDPDYPVTHNVPSPGIEQLPSQPSAPIASSPAIDMPPQSETISSPPQTHVSG 357  
Db 340 TA-----  
QY 358 TPPPVKASFSSTVTSAPANVNTSAPPVQTDIVNTSSISD--LENOVLQMEKALSLSLE 415  
Db 342 ---VKPAY-----VSFCAQIN-----NIFSLVDKVCENKTTVVSLKNTTESFV 381  
QY 416 PNLAGEMINQVSRLLHSPDMLAPLAQRLLKVVDIGLQNLNSNTTISLTPSLALAVIR 475  
Db 382 P-----VLKQISMWTKFTKEETSSLATVELESMTL-ASFWKPSANVT-PAVRAEYLD 434  
QY 476 VNASSFNITTFVAQDPANLOVSLQTAQENISGTTITLPSLMMNLPAHDMELASRVQFNF 535

MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-852-806-2

Query Match 7.7%; Score 411.5; DB 2; Length 1052;  
Best Local Similarity 25.9%; Pred. No. 2.9e-24;  
Matches 167; Conservative 99; Mismatches 233; Indels 145; Gaps 29;

QY 437 LAPLAQRLLKVDD-----IGLQNFNTTSLTSPSLALAVIR--VNASSFNTT-----484  
DB 187 VSPGSHLLRVVDEDFHLVGDALKAFQSSLLVTD-NLVISIQREPVSASSDITFPMRGR 245  
QY 485 -----TFVAQD-----PANLQVLETPQAPENSIGTITLPSLMNNLPAHDM 525  
DB 246 RGMKDWVRHSEDRFLPKEVLSSSPGKATSGAAGSPGRGPGCTVPPG-----PGHSH 300  
QY 526 EL---ASRVQNFETFPALFQDPSLENLSLI-----SYVSSSVANLTVRLNTRN---572  
DB 301 QRLLPADPDESSYFVIGAVL---YRTGLILPPRPPPLAVTSRVMTVTRPPTQPPAEP 356  
QY 573 -VTVTLLKH-INPSQDELTVRCVFDLGR-NGGRGWSNDGSCVKDRRLNETICTCSHLTS 629  
DB 357 LITVELSYIINGTTDP---HCASWDYSRADASSGDWDENCOTLETAHAHRCQOHLST 413  
QY 630 FGVL-----LDLSRTSVLPQAMMALFTITYGCGLSIFLSVTLTYIAFEKIRRDY 681  
DB 414 FAVLAQPPKDLTLELAGSPSV-----LVIGCAVSCMALLTLAIYAAFWRFIKSE 464  
QY 682 FSKILIQCAALLLNVLFLDLSWIALYKMOGLCISAVFLHYFLVFTWMLGLFAFHY 741  
DB 465 RSIILLNFCLSILASNILVVGOSRVLSK--GVCTMTAAFLHFFFLSCFWVLTEAWQSY 522  
QY 742 LALVKVNT-YIRKYLLKFCIVGWGPVAVVTVITLTIS-PDNYGLGSGKFPNGSPDDPC 799  
DB 523 LAVIGRMTRLVRK---RFLCGWGLPALVAVSVGTRTKGYGTSSY-----C 568  
QY 800 WINNAVFIYVVGFCVIFLLNVSMFIVVLVQLCR-----IKKKQLGAQRKTSIQDL 853  
DB 569 WLSLEGLLYAFVGPAAVIVLVNMLIGIIVFNKLMARDGIDSKSKQRAGA-----SL 621  
QY 854 RSIAGLTLLGTTWGFAPFAW-GPVNVTFMYLFAFNLTLOGFFIFIFYCVAKENVKQWR 912  
DB 622 WSSCVVLPALLTWTMSAVLAMTDRRSVLFQALFAVFNQAQGFVITAVHCF-----LRREVQ 677  
QY 913 RYLC--GKRLAENSQWKTATNG-----LKKQTVNOGVSSSSNSLOSSEN 957  
DB 678 DVYKQMGVCRASEDSDPSCKNGQLQILSDFEKQVDLACQTV---LFKEVNTCNPSTI 734  
QY 958 STNSTLLVNNND-----CSVHASGNGNASTERNGVSPSVQNGDV 996  
DB 735 TGTLSRLSDEDEPKSLCVGPBG-----LSFSPPLPGNI 769

RESULT 7

US-09-163-669-2  
Sequence 2, Application US/09163669  
Patent No. 611076  
GENERAL INFORMATION:  
APPLICANT: FUKUSUMI, SHOJI  
APPLICANT: HINUMA, SHOJI  
APPLICANT: FUJII, RYO  
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED  
RECEPTOR (HIBCD07)  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA

COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/163,669  
FILING DATE: 30-SEP-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/852,806  
FILING DATE: 07-MAY-1997  
APPLICATION NUMBER: 60/017,915  
FILING DATE: 16-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: TAK-50002-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0700  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1052 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-163-669-2

Query Match 7.7%; Score 411.5; DB 3; Length 1052;  
Best Local Similarity 25.9%; Pred. No. 2.9e-24;  
Matches 167; Conservative 99; Mismatches 233; Indels 145; Gaps 29;

QY 437 LAPLAQRLLKVDD-----IGLQNFNTTSLTSPSLALAVIR--VNASSFNTT-----484  
DB 187 VSPGSHLLRVVDEDFHLVGDALKAFQSSLLVTD-NLVISIQREPVSASSDITFPMRGR 245  
QY 485 -----TFVAQD-----PANLQVLETPQAPENSIGTITLPSLMNNLPAHDM 525  
DB 246 RGMKDWVRHSEDRFLPKEVLSSSPGKATSGAAGSPGRGPGCTVPPG-----PGHSH 300  
QY 526 EL---ASRVQNFETFPALFQDPSLENLSLI-----SYVSSSVANLTVRLNTRN---572  
DB 301 QRLLPADPDESSYFVIGAVL---YRTGLILPPRPPPLAVTSRVMTVTRPPTQPPAEP 356  
QY 573 -VTVTLLKH-INPSQDELTVRCVFDLGR-NGGRGWSNDGSCVKDRRLNETICTCSHLTS 629  
DB 357 LITVELSYIINGTTDP---HCASWDYSRADASSGDWDENCOTLETAHAHRCQOHLST 413  
QY 630 FGVL-----LDLSRTSVLPQAMMALFTITYGCGLSIFLSVTLTYIAFEKIRRDY 681  
DB 414 FAVLAQPPKDLTLELAGSPSV-----LVIGCAVSCMALLTLAIYAAFWRFIKSE 464  
QY 682 FSKILIQCAALLLNVLFLDLSWIALYKMOGLCISAVFLHYFLVFTWMLGLFAFHY 741  
DB 465 RSIILLNFCLSILASNILVVGOSRVLSK--GVCTMTAAFLHFFFLSCFWVLTEAWQSY 522  
QY 742 LALVKVNT-YIRKYLLKFCIVGWGPVAVVTVITLTIS-PDNYGLGSGKFPNGSPDDPC 799  
DB 523 LAVIGRMTRLVRK---RFLCGWGLPALVAVSVGTRTKGYGTSSY-----C 568  
QY 800 WINNAVFIYVVGFCVIFLLNVSMFIVVLVQLCR-----IKKKQLGAQRKTSIQDL 853  
DB 569 WLSLEGLLYAFVGPAAVIVLVNMLIGIIVFNKLMARDGIDSKSKQRAGA-----SL 621  
QY 854 RSIAGLTLLGTTWGFAPFAW-GPVNVTFMYLFAFNLTLOGFFIFIFYCVAKENVKQWR 912  
DB 622 WSSCVVLPALLTWTMSAVLAMTDRRSVLFQALFAVFNQAQGFVITAVHCF-----LRREVQ 677

QY 913 RYLCC--GKRLAENSWSKTATNG-----LKKQTVNQGVSSSSSLOSSN 957  
 Db 678 DVYKQMGVCRADESEDPSCCKNGQLQILSDFEKDVLACQTV---LFPKEVNTCPNSTI 734  
 QY 958 STNSTLLVNND-----CSVHASGNGNASTERNNGVSFSYQNGDV 996  
 Db 735 TGLSRSLUDEDEPKSLCVGPEG-----LSFSLPLGNI 769

RESULT 8  
 US-08-465-976A-2  
 ; Sequence 2, Application US/08465976A  
 ; Patent No. 5869632  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOPPET, DANIEL R  
 ; APPLICANT: LI, YI  
 ; APPLICANT: ROSEN, CRAIG A  
 ; APPLICANT: RUBEN, STEVEN M  
 ; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CARELLA, BYRNE, BAIN GILFILLAN, CECCHI  
 ; ADDRESSEE: STEWART & OLSTEIN  
 ; STREET: 6 BECKER FARM ROAD  
 ; CITY: ROSELAND  
 ; STATE: NJ  
 ; COUNTRY: US  
 ; ZIP: 07068  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/465.976A  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FERRARO, GREGORY F  
 ; REGISTRATION NUMBER: 36,134  
 ; REFERENCE/DOCKET NUMBER: 325800-444  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (201) 994-1700  
 ; TELEFAX: (201) 994-1744  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 884 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-465-976A-2

Query Match 6.9%; Score 367.5; DB 2; Length 884;  
 Best Local Similarity 25.2%; Pred. No. 7.7e-21;  
 Matches 127; Conservative 85; Mismatches 224; Indels 67; Gaps 15;

QY 560 SVANLTVRNLTRNVTVT-----LKHINPSODELTVRCVFW-D-LGRNGRGGSNDGC 610  
 Db 7 SVAVFHGRNFRGLGILESPISLEFRLLQTANRSK-----AICVQWDPPGLAQHGVWTARD 62

QY 611 SVKDRRLNETICTCSHLTSGVLLDLSTSVLPQAOMALTFIYICGLSSIFLSVTLVT 670  
 Db 63 ELVHRNGSHARCRCSTGTGFLMDASPRERLEGDLLELAVETHVVAVVAVAAVLTA 122

QY 671 YIAEKIRDPYPSKTLIQCALALLLNVLFDLSWTALKYMGGLCISVAVFHLHYLVSVF 730  
 Db 123 LLSRLSKSNVRG--THANVAAALGVAELFLIG--IHRTHNQLVCTAVALLLHYFFLSTF 179

QY 731 TWGLEAFMYLALVKVNTYIRKKILKFC--IVGWGVPVAVVTVIITISPNDYGLSGYK 789  
 Db 180 AWFVQGLHLYRMQVEPRN--VDRGAMFEYHALGNGVPAVLGLAVGLDPEGY-----230

QY 790 FPNGPSDDFCWNNNAVFIYTVVGYFCVIFLLNVSFMFIVVLVOLCRKKKKQLGAORKTS 849  
 Db 231 ---GNP-DFCWISVHEPLINSGAGPVVLVIVMNGTFLAARTSCSTGORE-----AKTS 282

QY 850 IQDLRSIAGLTFLLGITWGAFAFFAMGPVNVTFMYLFAIFNTLQGGFFIFIFCYVAKENVRK 909  
 Db 283 ALTURSSFLLLLVSASWLFGLLAVNHSILAFHYLHAGLCGLQGLAVLLFCVLNADARA 342

QY 910 QWRRYLCGCKLRLAENS-----DWSKTA---TNGLLKQTVNQGVSSSSSLSQS--- 954  
 Db 343 AWMP-ACLGRKAAPPEARPAPGLGFCAYNNLTALFEESGLIRITLGASTVSVSSARSGR 401

QY 955 -SSNSTNTTLLVNNDSCSVHASGNGNAS-----TERNGVSFSYQNGDV 997  
 Db 402 QDQDSQGRSYLRDNVLYRHGSAADHTDHSLOAHAGTDLDDVDMFHRDAGADSDSDLS 461

QY 998 LHDFGTGKOHMFNEKEDSCNGKGR 1020  
 Db 462 LEEERSLSIPSSSESDNGRTRGR 484

RESULT 9  
 US-08-982-412-2  
 ; Sequence 2, Application US/08982412  
 ; Patent No. 5958729  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOPPET, DANIEL R  
 ; APPLICANT: LI, YI  
 ; APPLICANT: ROSEN, CRAIG A  
 ; APPLICANT: RUBEN, STEVEN M  
 ; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
 ; STREET: 9410 KEY WEST AVENUE  
 ; CITY: ROCKVILLE,  
 ; STATE: MD  
 ; COUNTRY: US  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/982,412  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROOKES, ANDERS A  
 ; REGISTRATION NUMBER: 36,373  
 ; REFERENCE/DOCKET NUMBER: PF181PCT2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (301) 309-8504  
 ; TELEFAX: (301) 309-8439  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 884 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-982-412-2

Query Match 6.9%; Score 367.5; DB 2; Length 884;  
 Best Local Similarity 25.2%; Pred. No. 7.7e-21;  
 Matches 127; Conservative 85; Mismatches 224; Indels 67; Gaps 15;

QY 560 SVANLTVRNLTRNVTVT-----LKHINPSODELTVRCVFW-D-LGRNGRGGSNDGC 610  
 Db 7 SVAVFHGRNFRGLGILESPISLEFRLLQTANRSK-----AICVQWDPPGLAQHGVWTARD 62



; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 231  
; TYPE: PRP  
; ORGANISM: Homosapiens  
US-09-370-098-4

Query Match 4.6%; Score 245.5; DB 4; Length 231;  
Best Local Similarity 27.5%; Pred. No. 5.9e-12;  
Matches 71; Conservative 48; Mismatches 96; Indels 43; Gaps 9;

QY 661 SIP-LSVTLVYIAFEKIRRDYPSKILQICAAALLNLVFLDLSWIALYKMOG-----L 714  
DB 1 SIFCLLLCILTFLVLPQGS-RTTHLHCICLIFVGSITFL-----AGIENEGQVGLR 54  
QY 715 CISVAVFLHYFLVSTWMLGFHMYLALVKVF--NTYIRKYLKFCIVGVGVPVAVVT 772  
DB 55 CRIVAGLLHYCGLAAGCWSLEGLFLVVRVFGQGLSTRWL---CLIGYGVPLLIWG 111  
QY 773 IILTISPDNVLGSLGKFPNGSPDDFCWNNNAVYITVVCYFVIFLLNVSMFTVVLVQ 832  
DB 112 VSAIYSKGVGRPY-----CWLDFEQGLWSFLGPTVFIILCNVIFVTTVMK 160  
QY 833 LCR-----IKKKQLGAKRKTSIQDLRSIAGLTFLGTTWGAFAFFWGPVNVTFMYL 884  
DB 161 LTKQFSEINPDMKKLKKARALTITAIQAQ-----FLGCTWVFGLEFDDRSVLVTV 213  
QY 885 FAIFNTLQGFIFIFVCV 902  
DB 214 FTILNCLOGAFLYLLHCL 231

## RESULT 13

US-08-811-897A-56  
; Sequence 56, Application US/08811897A  
; Patent No. 5858787  
; GENERAL INFORMATION:  
; APPLICANT: ONDA, Haruo  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: KITADA, Chieko  
; APPLICANT: ISHIBASHI, Yoshihiro  
; APPLICANT: HOSoya, Masaki  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: MIYAMOTO, Yasunori  
; APPLICANT: HABATA, Yugo  
; APPLICANT: SHIMAMOTO, No. 5858787io  
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING  
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/811,897A  
; FILING DATE: 05-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/202,986  
; FILING DATE: February 25, 1994  
; ATTORNEY/AGENT INFORMATION:

; NAME: RESNICK, David S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 44168-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1324 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-811-897A-56

Query Match 4.5%; Score 240.5; DB 2; Length 1324;

Best Local Similarity 22.9%; Pred. No. 2.5e-10;  
Matches 109; Conservative 77; Mismatches 178; Indels 111; Gaps 20;

QY 594 WDLGRNGRGGWSD-----NGCSVKDRRLNETICTCSHLTSFGVLLDLSTSVLP AQM 646  
DB 101 YNISRSCTEGWSQLEPGYHIACGLND-----RASSLDEQ 137  
QY 647 MALTFIY-----IGGLSSIFSLVTLVYIAFEKIR--RDYPSKILQICAAALLNLV 699  
DB 138 QTKFYNTVKTGYTIGYSLSLASLLVAMAILSLFRKLHCTRNVIHMLFW--SFLRATAV 195  
QY 700 FLDSWIALYKMOGL-----CISVAVFLHYFLVSTWMLGFHMYLALVKVFNT 750  
DB 196 FIRD--MALFNSGEIDHCSEASVGCNAVVFQYCVMAFFWLLVEGLYLYTLAVSFFS 253  
QY 751 YIRKYLKFCIVGVGVPVAVVTI--ILTISPDNVLGSLGKFPNGSPDDFCW--INNAV 806  
DB 254 E-RKYFWGYILIGWVPSVFTITVTVRIYFEDFG-----CWDTIINSSL 297  
QY 807 FYITVVGVCVIFLLNVSMFTVVLVQLCRKKKKGAKRKTSIQDLRSIAGLTFLGIT 866  
DB 298 WWI--IKAPILLSILNVFVIFICIIRILYOKLRPPDIG---KNDSSPYSLAKSTLLIPL 353  
QY 867 WG--FAPFAGPWNV--TFMYLFAIFNTLQGFIFIFVCV---AKENVKQWRRLCC 917  
DB 354 FGIHYVMFAFPDNFKAQVKMVFELVVGSGFQGVVAILCYFLNGEVOAELRRKWRWHLQ 413  
QY 918 GKRLAENSWSKATNGLKKQTQVNGVSSSSNSLQSSNSNSTNTLLVN-----NDCSV 972  
DB 414 GVLGWSKSKQHPWGGSGNGATCSTQVSMLTRVSPSARRSS-SFOAEVSLVNHADPFNBCWI 472  
QY 973 HASNGNASTERNGVSVFQVQNGDVCLHDFGTGKOHMFENEKEDSCNGKRMALRRTS 1027  
DB 473 N-----DWSTE-----MPARDNASEQENCEDGTNRSAMRPPS 505

## RESULT 14

US-08-811-897A-18  
; Sequence 18, Application US/08811897A  
; Patent No. 5858787  
; GENERAL INFORMATION:  
; APPLICANT: ONDA, Haruo  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: KITADA, Chieko  
; APPLICANT: ISHIBASHI, Yoshihiro  
; APPLICANT: HOSoya, Masaki  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: MIYAMOTO, Yasunori  
; APPLICANT: HABATA, Yugo  
; APPLICANT: SHIMAMOTO, No. 5858787io  
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING  
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN



Db 278 dstiskvipgngklll-----gsnqneivslkgdiynfrlwnftmnakilsnlsncvkn 332  
 Qy 124 -----VKPQRNI-----CNLSSICNDSAPFRGEIMFQY 151  
 Db 333 vvdqndfwnlpnlaikaesnlsccgsvlipaaelaascadltcqdgiyrisvviq- 391  
 Qy 152 DKESTVPQNHITNGTLTGLVLSLSEKRS-----LNKTLTSETYFIMCATAEAQSTL 206  
 Db 392 -----nllrpevkqsvaewlnstfgwnyvyv-----v 423  
 Qy 207 NCTFTIKLNTMNACAAIALERVKIRPMEHCCSVRIPCSPPEELGKL----- 256  
 Db 424 nlsfnls-----agedkikvk-----rsledeprlviallvyna 458  
 Qy 257 --QCLOQDPIVCLADHPRGPPFSSQSIPVVPVPRATVLS--QVPKATSPAEPDPDYSPVTHN 312  
 Db 459 tntnlegkii-----qkllknnesldeglrlhtvnrqlghclameepkgy-----y 507  
 Qy 313 VPSPIGEIQP--LSPQPSAPIASSPAIDMPPQSETISSPMPQTHVSGTPTPPPVKASFSSP 369  
 Db 508 wps-----iqpseyvlpcdpkpgfsasri-----cfynatnplv----- 541  
 Qy 370 TVSAPANVNT--TSAPPVQDIDVNTS-----SISDLENQVLOMEKALS-OSLEPNLAG 420  
 Db 542 tywgpvdiansclkeanevanqilnltadggnltseanitniveqvkrievkeenniditlgs 601  
 Qy 421 EMINQVSRLLKSPDMLAPLQRLKVVDDIGLOLNFSTT- ISLTSPSLALAVIRVNAS 479  
 Db 602 timnifsnlssdsdlsessealktldelafkidlnstshvnttrnlaisvsallpg 661  
 Qy 480 SPNTTTFVAQDPAN---LOVSLTQAPENSIGITLTPSSLMNNLPAHDMELASRVQFNF 535  
 Db 662 tnaishfsglpsnnesyfgmdfes-gqvdpilasvilppnllenispedsvlvrraqftf 720  
 Qy 536 FETPALFQDPSLENLSLISVSSVANLTVRNLTNRVTTLKHINPSODELTVCVFEWD 595  
 Db 721 fktglfdvgpqrktlsvymacsigitnqkdpvqikkkhtrtqevhhpi-cafwd 779  
 Qy 596 LGRNGRGGSWSDNGC-SVKDRRLNETICTCSHLTSFGVLLDLSRT-SVLPQAQ-MMALTFI 652  
 Db 780 lnnksgfgwntsgcvahrdsdasetvclcnhfhfvgvLmdlprsasqldarntkvtfl 839  
 Qy 653 TYIGCGLSIFLSVTLTYTAFEXIRDRDPSKILLQLCALLLNLVFLDLSWIALYKMQ 712  
 Db 840 syigcisaifsaatlityvafeklrdrdpskilmnlstallnllfldgwitsfnvd 899  
 Qy 713 GLCISVAVFLHYFLVSVFTWGLEAFHMYLALVKVFNTRYIRKYILKFCIVGCVPAVVVT 772  
 Db 900 glciavavllhffllatftwmgleaahmyialkvfntryirylkfcigqpalvvs 959  
 Qy 773 ILTISPDN--YGLGSYGKPNPSPDPFCWINNNNAVFTYVVGVFCVIFLLNVSMFIVVL 830  
 Db 960 vvlasrnnnevygkesyjk---ekgdefcwiqdpvifvycagfygvmfllniamfivvm 1016  
 Qy 831 VOLCRKIKKQLQAQRKTSLODLRSIAGLTLLGTTGTFAPFAFGVPVNVTEMYLEAFINT 890  
 Db 1017 vqicgrngkrnsrntllreevlnrsvslftllgmtwgfaffawgplnlpfmylfsifns 1076  
 Qy 891 LOG 893  
 Db 1077 lqg 1079

Search completed: May 23, 2002, 07:37:55  
 Job time: 160 sec

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; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,897A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-811-897A-18

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Query Match 4.4%; Score 233; DB 2; Length 448;  
 Best Local Similarity 23.2%; Pred. No. 1.7e-10;  
 Matches 92; Conservative 75; Mismatches 145; Indels 84; Gaps 19;

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QY 596 LGRNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGVLLDLSRTSVLPQMMAL 649
Db 94 VGRNCTEDGWSEPPPHYFACGDDYE-----PESGDQDYIYLSV 133
QY 650 TFIYVIGCGLSIFSLVTLVYIAFEKIR--RDYPSKILIOALCAALLNLVFLDLSWA 707
Db 134 KALYTVGVSTSLATLTAMVILCRFKLHCTRNF---IHMNLFVSMFLRAISVFKDWI- 189
QY 708 LYKMOGL-----CISVAVFLHYFLVSTWMLGAEAFHMYLALVKVFNTRYIRKYILK 758
Db 190 LYAEOSSHCFSVTECKAVMVFHYCVVSNYFWLFTGLYLFETLLVETFPPE--RRYFW 248
QY 759 FCIVGWGPVAVVTI--ILTISPDNYGLSGYKFPNGSPDDFCWINNN--AVFYI---TV 811
Db 249 YTIIGWGTPVTCVTVMVRLYFDDAG-----CWDMDNSTALWVYIKGPV 293
QY 812 VGYFCVIFLLNVSMFIVLQVLCRIKKKOLGAQRKTSIODLRSIAGLTFLLGITWGEAF 871
Db 294 VGSIMNVFLVFI--IIILVQ--KLOSPDMGNGESSIYLRARSTLLIPLFGI--HTV 348
QY 872 FAWGPVNVVT--FMYLFAI--FNTLQGFIFIFYCV-----AKENVRKQWRRYLCCGKRLAE 924
Db 349 FAFSPENYSKRERLVFELGLSGFQGPVAVLYCFNGEVOAEIKKWRSW---KVNRYF 404
QY 925 NSDWS-----KATNGLKKQTQVNGVSSSSNSLQSSS 956
Db 405 TMDFKRHPSSLASSGVNGTQLSILSKSSQLRMSS 440

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RESULT 15  
 US-08-855-213-18  
 ; Sequence 18, Application US/08855213  
 ; Patent No. 5892004  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ONDA, Haruo  
 ; APPLICANT: OHTAKI, Tetsuya

```

; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 589200410
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR
; PREPARING SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,213
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-855-213-18

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Query Match 4.4%; Score 233; DB 2; Length 448;  
 Best Local Similarity 23.2%; Pred. No. 1.7e-10;  
 Matches 92; Conservative 75; Mismatches 145; Indels 84; Gaps 19;

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QY 596 LGRNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGVLLDLSRTSVLPQMMAL 649
Db 94 VGRNCTEDGWSEPPPHYFACGDDYE-----PESGDQDYIYLSV 133
QY 650 TFIYVIGCGLSIFSLVTLVYIAFEKIR--RDYPSKILIOALCAALLNLVFLDLSWA 707
Db 134 KALYTVGVSTSLATLTAMVILCRFKLHCTRNF---IHMNLFVSMFLRAISVFKDWI- 189
QY 708 LYKMOGL-----CISVAVFLHYFLVSTWMLGAEAFHMYLALVKVFNTRYIRKYILK 758
Db 190 LYAEOSSHCFSVTECKAVMVFHYCVVSNYFWLFTGLYLFETLLVETFPPE--RRYFW 248
QY 759 FCIVGWGPVAVVTI--ILTISPDNYGLSGYKFPNGSPDDFCWINNN--AVFYI---TV 811
Db 249 YTIIGWGTPVTCVTVMVRLYFDDAG-----CWDMDNSTALWVYIKGPV 293
QY 812 VGYFCVIFLLNVSMFIVLQVLCRIKKKOLGAQRKTSIODLRSIAGLTFLLGITWGEAF 871
Db 294 VGSIMNVFLVFI--IIILVQ--KLOSPDMGNGESSIYLRARSTLLIPLFGI--HTV 348
QY 872 FAWGPVNVVT--FMYLFAI--FNTLQGFIFIFYCV-----AKENVRKQWRRYLCCGKRLAE 924

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Db 349 FAFSPENVRERLVLFGELGSGFGVAVLYCFLNGEVAQAEIKRKRWSW-----KVNRYF 404  
QY 925 NSDWS-----KTAATNGLKKQTQVNOQGVSSSSNSLSQSSS 956  
Db 405 TMDFKHRHPSLASSGVNGGTQLSLSKSSSSQLRMSS 440

## RESULT 16

US-08-811-897A-19  
; Sequence 19, Application US/08811897A  
; Patent No. 5858787  
; GENERAL INFORMATION:  
; APPLICANT: ONDA, Haruo  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: KITADA, Chieko  
; APPLICANT: ISHIBASHI, Yoshihiro  
; APPLICANT: HOSOYA, Masaki  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: MIYAMOTO, Yasunori  
; APPLICANT: HABATA, Yugo  
; APPLICANT: SHIMAMOTO, No. 5858787io  
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING  
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/811.897A  
; FILING DATE: 05-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/202,986  
; FILING DATE: February 25, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, David S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 44168-DIV  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-811-897A-19

Query Match 4.4%; Score 233; DB 2; Length 467;  
Best Local Similarity 23.2%; Pred. No. 1.9e-10;  
Matches 92; Conservative 75; Mismatches 145; Indels 84; Gaps 19;

QY 596 LGRNGRGGWS-----NGCSVKDRRLNETTCTGSHLTSGVLLDLSTVSLPAQMML 649  
Db 113 VGRNCTEDGSEPFPHYDFACGFDYE-----PESGDQDYIYLSV 152  
QY 650 TFIYVIGGLSIFSLVLTVAIEAKIR--RDYPSKILQICALLLNVLFLDLSWIA 707  
Db 153 KALYTVGYSTSLATLTATNVLRCRFLKCHTNP----IHMNLFVSPMLRAISVFIKDWI- 208

QY 708 LYKMOGL-----CISVAVFLHYFLVSVFTWGLEAFHMYLALVKVENTYIRKYLK 758  
Db 209 LYAQDSSSHCFVSTECKAVAVFFHYCVVSNYFWLFIEGLYFLTLVETFFPE--RRVEYW 267  
QY 759 FCYVGWGPVAVVVTI--ILTISPDNYGLSGYKFPNGSPDPCFWINN--AVFYI---TV 811  
Db 268 YTIIGWGTPVTCVTWAVLRLYFDDAG-----CWDMDSTALWVVIKGPV 312  
QY 812 VGYFCVIFLLNVSMEIVVLQCRILKKKQKQALGAQRKTSIQLRSIAGLTFLGLGITWGF 871  
Db 313 VGSIMVNFVFIGI--IILVQ--KLQSPDMGNNESSIYLRKARSTLLIPLFGI--HYTV 367  
QY 872 FAWGPVNVVT--FMYLFAI--FNTLOGFFIFIFYCV-----AKENVRKQWRRYLCCGKRLAE 924  
Db 368 FAFSPENVRERLVLFGELGSGFGVAVLYCFLNGEVAQAEIKRKRWSW-----KVNRYF 423  
QY 925 NSDWS-----KTAATNGLKKQTQVNOQGVSSSSNSLSQSSS 956  
Db 424 TMDFKHRHPSLASSGVNGGTQLSLSKSSSSQLRMSS 459

## RESULT 17

US-08-855-213-19  
; Sequence 19, Application US/08855213  
; Patent No. 5892004  
; GENERAL INFORMATION:  
; APPLICANT: ONDA, Haruo  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: KITADA, Chieko  
; APPLICANT: ISHIBASHI, Yoshihiro  
; APPLICANT: HOSOYA, Masaki  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: MIYAMOTO, Yasunori  
; APPLICANT: HABATA, Yugo  
; APPLICANT: SHIMAMOTO, No. 5892004io  
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR  
; TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/855,213  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/202,986  
; FILING DATE: 25-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, David S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 44168  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-855-213-19

Query Match 4.4%; Score 233; DB 2; Length 467;  
Best Local Similarity 23.2%; Pred. No. 1.9e-10;  
Matches 92; Conservative 75; Mismatches 145; Indels 84; Gaps 19;

QY 596 LGRNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGVLDLSRTSVLPQAQMMAL 649  
DB 113 VGRNCTEDGSEPPFPYDAGCFDDYE-----PESGDQDYYYSV 152  
QY 650 TFIYIGGLSIFSVTLVTYIAFEKIR--RDYPSKILQLCAALLNLNLFVLDWSIA 707  
DB 153 KALYTVGYSTSLATLTAMVILCRFKLHCTRNF---IHMNLVFSFMLRAISVFIKDWI- 208  
QY 708 LYKMQGL-----CISVAVFLHYFLVSVFTWGLEAFHMYLALVKVFTYIRKYILK 758  
DB 209 LYAEQDSHCFVSTVECKAVMFFHYCVVSNFYFWLFIEGLYFLFTLLVETFPPE-RRYFYW 267  
QY 759 FCIVGWGVPVAVVTI--ILTISPNDNYGLSGYKFPNGSPDDFCWINNN--AVEYI---TV 811  
DB 268 YTIIGWGPTVCVTWAVLRYFDAG-----CWDMDSTALWVWIKGPV 312  
QY 812 VGYFCVIFLLNVSMFIVVLQCRKKKKKOLGAQRKTSIODLRSIAGLTFLLGITWGF 871  
DB 313 VGSIMVNFVFIGI-IIIIVQ--KLQSPDMGNGNESSIYLRLARSTLLIPLFGI--HYTV 367  
QY 872 FAWGPVNVV--FMYLFAI--FNTLQGFIFIFVCV---AKENVRKWRRLYLCCKGLRLAE 924  
DB 368 FAFSPENVSKRERLVFELGLSGFSQGFVAVVLCFLNGEVAQAEIKRWSW---KVNRYF 423  
QY 925 NSDWS----KTATNGLKKQTVNQGVSSSSNSLQSS 956  
DB 424 TMDPKRHRPSLASSGVNGTQLSILSKSSQLRMSS 459

## RESULT 18

US-08-811-897A-16

Sequence 16, Application US/08811897A  
Patent No. 5858787  
GENERAL INFORMATION:  
APPLICANT: ONDA, Haruo  
APPLICANT: OHTAKI, Tetsuya  
APPLICANT: MASUDA, Yasushi  
APPLICANT: KITADA, Chieko  
APPLICANT: ISHIBASHI, Yoshihiro  
APPLICANT: HOSOYA, Masaki  
APPLICANT: OGI, Kazuhiro  
APPLICANT: MIYAMOTO, Yasunori  
APPLICANT: HABATA, Yugo  
APPLICANT: SHIMAMOTO, No. 5858787io  
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING  
TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
ADDRESS: CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/811.897A  
FILING DATE: 05-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/202,986  
FILING DATE: February 25, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, David S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 44168-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 448 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-811-897A-16

Query Match 4.3%; Score 231.5; DB 2; Length 448;  
Best Local Similarity 21.8%; Pred. No. 2.3e-10;  
Matches 103; Conservative 88; Mismatches 165; Indels 117; Gaps 23;

QY 521 PAH--DMELASRVQ--FNFETPALFQDPSLENLSLISYVSSSVANLTVRLNRVTVL 577  
DB 46 PAHVGMVLSVPELFRIFNPQVWE---TETIGFQFADSKSLDLSMDRVVSRNCT--- 99  
QY 578 KHINPSODELTVRCVFDLGRNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGF 631  
DB 100 -----EDGWSEPPFPYDAGCFEYE----- 120  
QY 632 VLDDLSRTSVLPQAQMMALTFIYIGGLSIFLSVTLVTYIAFEKIR--RDYPSKILQL 689  
DB 121 ----SETGDQDYYVLSVKALYTVGYSTSLVTLTAMVILCRFKLHCTRNF---IHMNL 172  
QY 690 CAALLLNLFVLDWSIALYKMQGL-----CISVAVFLHYFLVSVFTWGLEAFHM 740  
DB 173 FVSPMLRAISVFIKDWI--LYAEQDSNHCFVSTVECKAVMFFHYCVVSNFYFWLFIEGLY 231  
QY 741 YLALVKVFNVTYIRKYILKFCIVGWGVPVAVVTI--ILTISPNDNYGLSGYKFPNGSPDF 798  
DB 232 FTLLVETFPPE-RRYFYWIIIGWGTPTVCVSWVAMRLYFDGTG----- 275  
QY 799 CW--INNNAVEYI---TVVGYFCVIFLLNVSMFIVVLQCRKKKKOLGAQRKTSIODL 853  
DB 276 CWDMDNTALWVWIKGPVVGSIWVNFVFIGI-IIIIVQ--KLQSPDMGNGNESSIYLRLA 332  
QY 854 RSIAGLTFLLGITWGFQFAFANGCPVNVV--FMYLFAI--FNTLQGFIFIFVCV---AKEN 906  
DB 333 RSTLLIPLFGI--HYTVFAFSPENVSKRERLVFELGLSGFSQGFVAVVLCFLNGEVAQAE 390  
QY 907 VRKWRRLYLCCKGLRLAEVSDWS----KTATNGLKKQTVNQGVSSSSNSLQSS 955  
DB 391 IKRWRWSW---KVNRYFTMDFKRHRPSLASSGVNGTQLSILSKSSQIRMS 439

## RESULT 19

US-08-855-213-16  
Sequence 16, Application US/08855213  
Patent No. 5892004  
GENERAL INFORMATION:

APPLICANT: ONDA, Haruo  
APPLICANT: OHTAKI, Tetsuya  
APPLICANT: MASUDA, Yasushi  
APPLICANT: KITADA, Chieko  
APPLICANT: ISHIBASHI, Yoshihiro  
APPLICANT: HOSOYA, Masaki  
APPLICANT: OGI, Kazuhiro  
APPLICANT: MIYAMOTO, Yasunori  
APPLICANT: HABATA, Yugo  
APPLICANT: SHIMAMOTO, No. 5892004io  
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR  
TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF  
NUMBER OF SEQUENCES: 55



Db 210 FVSMRLRAISVFIKDWI-LXAEQDSNHCFSVSTVECKAVMVFHYCVVSNFYFWLFIKGLYL 268  
 QY 741 YLALVKVFNTRYIRKYLKFCIVGWPVAVVTI--ILTSPDNYGLSGYKFPNGSPDDF 798  
 Db 269 FTLLVETFEPE--RRFYFYWYIIIGWGTTCVCSVWMLRLYFDG----- 312  
 QY 799 CW--INNNAVFI---TVVGYFCVIFLLNYSMFIVLVQLCRKIKKKQLGAQRKTSIQDL 853  
 Db 313 CWDMDNTALMWVKGVPVGSIMVNFVFIGI-IVILVQ--KLQSPDMGNGESSIYLRLA 369  
 QY 854 RSIAGLTLLGWTGFAFFAWGPVNV--FMYLFAI-FNTLQGFIFIFYCV-----AKEN 906  
 Db 370 RSTLLIPLFGI--HYTVFAFSPENSKRRLVFLGSGFQGVVAVLYCFLNGEVQAE 427  
 QY 907 VRKQWRYLCCGKLRLAENSQWS-----KTATNGLKKQTVNOGVSSSSSSLOSS 955  
 Db 428 IKRWRSW---KVNRYFTMDFKRRHPSLASSGVNGGTQLSILSKSSQIRMS 476

RESULT 21  
 US-08-855-213-17  
 : Sequence 17, Application US/08855213  
 : Patent No. 5892004  
 : GENERAL INFORMATION:  
 : APPLICANT: ONDA, Haruo  
 : APPLICANT: OHTAKI, Tetsuya  
 : APPLICANT: MASUDA, Yasushi  
 : APPLICANT: KITADA, Chieko  
 : APPLICANT: ISHIBASHI, Yoshihiro  
 : APPLICANT: HOSoya, Masaki  
 : APPLICANT: OGI, Kazuhiro  
 : APPLICANT: MIYAMOTO, Yasunori  
 : APPLICANT: HABATA, Yugo  
 : APPLICANT: SHIMAMOTO, No. 58920041o  
 : TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR  
 : PREPARING SAID PROTEIN, AND USE THEREOF  
 : NUMBER OF SEQUENCES: 55  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
 : ADDRESSEE: CUSHMAN  
 : STREET: 130 Water Street  
 : CITY: Boston  
 : STATE: Massachusetts  
 : COUNTRY: US  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent in Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/855,213  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/202,986  
 : FILING DATE: 25-FEB-1994  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: RESNICK, David S.  
 : REGISTRATION NUMBER: 34235  
 : REFERENCE/DOCKET NUMBER: 44168  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617)523-3400  
 : TELEFAX: (617)523-6440  
 : TELEX: 200291 STRE UR  
 : INFORMATION FOR SEQ ID NO: 17:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 485 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-855-213-17

Query Match 4.3%; Score 231.5; DB 2; Length 485;  
 Best Local Similarity 21.8%; Pred. No. 2.6e-10;  
 Matches 103; Conservative 88; Mismatches 165; Indels 117; Gaps 23;  
 QY 521 PAH--DMELASRYQ-FNEFFETPALFQDFSLNLSLSVSVSSVANLTVRNLTRNVTVTL 577  
 Db 83 PAHVGEWLVSCPELFRIFNPQVWE---TETIGFEGADSKSLDSMDRVSRNCT--- 136  
 QY 578 KHINPSQDELTVRCVFWDLGRNGRGGWSD-----NGCSVKDRRLNETICTCSHLTSFG 631  
 Db 137 -----EDGWSPEPFHYFDACGFEEYE----- 157  
 QY 632 VLLDLSTRSVLPQAMMALTFITYIGCGLSIFSLVTLTYTAFKIR--RDYPSKILIQ 689  
 Db 158 -----SETGDQDYYSVKALYTVGYSTSLVTLTAMVILCFRKLHCTRNF---IHMNL 209  
 QY 690 CAALLLNLFVLDLSWIALYKMOGL-----CISVAVFLHYFLVFTWMLGFAFM 740  
 Db 210 FVSEMLRAISVFIKDWI-LXAEQDSNHCFSVSTVECKAVMVFHYCVVSNFYFWLFIKGLYL 268  
 QY 741 YLALVKVFNTRYIRKYLKFCIVGWPVAVVTI--ILTSPDNYGLSGYKFPNGSPDDF 798  
 Db 269 FTLLVETFEPE--RRFYFYWYIIIGWGTTCVCSVWMLRLYFDG----- 312  
 QY 799 CW--INNNAVFI---TVVGYFCVIFLLNYSMFIVLVQLCRKIKKKQLGAQRKTSIQDL 853  
 Db 313 CWDMDNTALMWVKGVPVGSIMVNFVFIGI-IVILVQ--KLQSPDMGNGESSIYLRLA 369  
 QY 854 RSIAGLTLLGWTGFAFFAWGPVNV--FMYLFAI-FNTLQGFIFIFYCV-----AKEN 906  
 Db 370 RSTLLIPLFGI--HYTVFAFSPENSKRRLVFLGSGFQGVVAVLYCFLNGEVQAE 427  
 QY 907 VRKQWRYLCCGKLRLAENSQWS-----KTATNGLKKQTVNOGVSSSSSSLOSS 955  
 Db 428 IKRWRSW---KVNRYFTMDFKRRHPSLASSGVNGGTQLSILSKSSQIRMS 476

RESULT 22  
 US-08-811-897A-20  
 : Sequence 20, Application US/08811897A  
 : Patent No. 5858787  
 : GENERAL INFORMATION:  
 : APPLICANT: ONDA, Haruo  
 : APPLICANT: OHTAKI, Tetsuya  
 : APPLICANT: MASUDA, Yasushi  
 : APPLICANT: KITADA, Chieko  
 : APPLICANT: ISHIBASHI, Yoshihiro  
 : APPLICANT: HOSoya, Masaki  
 : APPLICANT: OGI, Kazuhiro  
 : APPLICANT: MIYAMOTO, Yasunori  
 : APPLICANT: HABATA, Yugo  
 : APPLICANT: SHIMAMOTO, No. 58587871o  
 : TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING  
 : SAID PROTEIN, AND USE THEREOF  
 : NUMBER OF SEQUENCES: 56  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
 : ADDRESSEE: CUSHMAN  
 : STREET: 130 Water Street  
 : CITY: Boston  
 : STATE: Massachusetts  
 : COUNTRY: US  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM compatible  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FastSeq for Windows Version 2.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/811,897A  
 : FILING DATE: 05-MAR-1997  
 : CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-811-897A-20

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Query Match          4.3%; Score 231; DB 2; Length 476;
Best Local Similarity 22.6%; Pred. No. 2.8e-10;
Matches 95; Conservative 74; Mismatches 146; Indels 106; Gaps 20;

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QY 596 LGRNGRGGWSD-----NGSVKDRRLNETICTCSHLTSGVLLDLSTSVLPQAQMMAL 649
Db 94 VGRNCTEDGSEPPHYFDACGDDYE-----PESGDQDYVYLSV 133
QY 650 TFIYIGGLSIFLSVTLVYIAFEKIR--RDYPSKILQICALLLLNLVFLDLSWIA 707
Db 134 KALYTVGYSTSLATLTAMVILCRFRKLHCTRN-----IHMNLFVSMFLRAISVFIKDWI- 189
QY 708 LYKMOGL-----CISVAVFLHYFLVFTWGMGLEAFHMYLALVKVNTYIRKYILK 758
Db 190 LYAQDSSHCHFSVTECKAVMVFHYCVVSNFYFLFIEGLYFTLLVETFPPE-RRYFYW 248
QY 759 FCIVGWGVPVAVVTI--ILTISPNDYGLSGYKFPNGSPDDFCWINNN--AVFYI---TV 811
Db 249 YTIIGWGTPVCTVWVAVLRYLFDAG-----CWMNDSTALWVVIKGPV 293
QY 812 VGYFCVFLNVSMTFVL-----VOLCRIRKKKQKLAQRKTSIQD 852
Db 294 VGSIMVNFVFIIGIILVQKQSPDMGNGNESSIYFSCVQKCYC--KPQRAQOHSCKMSE 351
QY 853 LRSL-----AGLTFLLGITWG--FAFFANGPVNVT--FMYLFAI-FNTLQGFIFIFYCV- 902
Db 352 LSTITLRLARSTLLPLFGLIHVTFVAFSPENVSKRELVEFELGSGFQGVVAVLYCFL 411
QY 903 ---AKENVKQWRRYLCCGKRLAENSQWS---KTATNGLKQTVNOGVSSSSNSLOSS 955
Db 412 NGEVOAEIKRWRSW----KVNRYFTMDFKHRHPSLASSGVNGGTQLSILSKSSQLRMS 467
QY 956 S 956
Db 468 S 468

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```

RESULT 23
US-08-855-213-20
; Sequence 20, Application US/08855213
; Patent No. 5892004
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 589200410
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR
; TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF

```

```

; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ATTORNEY/AGENT INFORMATION:
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,213
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-855-213-20

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```

Query Match          4.3%; Score 231; DB 2; Length 476;
Best Local Similarity 22.6%; Pred. No. 2.8e-10;
Matches 95; Conservative 74; Mismatches 146; Indels 106; Gaps 20;

```

```

QY 596 LGRNGRGGWSD-----NGSVKDRRLNETICTCSHLTSGVLLDLSTSVLPQAQMMAL 649
Db 94 VGRNCTEDGSEPPHYFDACGDDYE-----PESGDQDYVYLSV 133
QY 650 TFIYIGGLSIFLSVTLVYIAFEKIR--RDYPSKILQICALLLLNLVFLDLSWIA 707
Db 134 KALYTVGYSTSLATLTAMVILCRFRKLHCTRN-----IHMNLFVSMFLRAISVFIKDWI- 189
QY 708 LYKMOGL-----CISVAVFLHYFLVFTWGMGLEAFHMYLALVKVNTYIRKYILK 758
Db 190 LYAQDSSHCHFSVTECKAVMVFHYCVVSNFYFLFIEGLYFTLLVETFPPE-RRYFYW 248
QY 759 FCIVGWGVPVAVVTI--ILTISPNDYGLSGYKFPNGSPDDFCWINNN--AVFYI---TV 811
Db 249 YTIIGWGTPVCTVWVAVLRYLFDAG-----CWMNDSTALWVVIKGPV 293
QY 812 VGYFCVFLNVSMTFVL-----VOLCRIRKKKQKLAQRKTSIQD 852
Db 294 VGSIMVNFVFIIGIILVQKQSPDMGNGNESSIYFSCVQKCYC--KPQRAQOHSCKMSE 351
QY 853 LRSL-----AGLTFLLGITWG--FAFFANGPVNVT--FMYLFAI-FNTLQGFIFIFYCV- 902
Db 352 LSTITLRLARSTLLPLFGLIHVTFVAFSPENVSKRELVEFELGSGFQGVVAVLYCFL 411
QY 903 ---AKENVKQWRRYLCCGKRLAENSQWS---KTATNGLKQTVNOGVSSSSNSLOSS 955
Db 412 NGEVOAEIKRWRSW----KVNRYFTMDFKHRHPSLASSGVNGGTQLSILSKSSQLRMS 467
QY 956 S 956
Db 468 S 468

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## RESULT 24

US-08-811-897A-21  
; Sequence 21, Application US/08811897A  
; Patent No. 5858787  
; GENERAL INFORMATION:  
; APPLICANT: ONDA, Haruo  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: KITADA, Chieko  
; APPLICANT: ISHIBASHI, Yoshihiro  
; APPLICANT: HOSoya, Masaki  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: MIYAMOTO, Yasunori  
; APPLICANT: HABATA, Yugo  
; APPLICANT: SHIMAMOTO, No. 5858787io  
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING  
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/811,897A  
; FILING DATE: 05-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/202,986  
; FILING DATE: February 25, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, David S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 44168-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 495 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-811-897A-21

Query Match 4.3%; Score 231; DB 2; Length 495;  
Best Local Similarity 22.6%; Pred. No. 3e-10;  
Matches 95; Conservative 74; Mismatches 146; Indels 106; Gaps 20;  
  
QY 596 LGRNGRGWSD-----NCCSVKDRRLNETICTSHLTSGVLLDLSTSVLPQMMAL 649  
Db 113 VGRNCTDQWSEFPFHYFDACGDYD-----PESGDQDYIYLSV 152  
  
QY 650 TPITYIGCLSLIFSVLTIVYIAFEKIR--RDYPSKILICLAALLLNLFVLLDSWTA 707  
Db 153 KALYTVGYSTSLATLTAMVILCRFKLHTRNF--IHMNLFVSMFLRAISVFIDWL- 208  
  
QY 708 LYKMOGL-----CISVAVFLHYLVSTWGLFAFHMVLAIVKVFYIRKYILK 758  
Db 209 LYAEQDSSCHFCSTVECKAVMVFHYCVSVNFWFLFIEGLVFLTLVETFFPE-RRYFYW 267  
  
QY 759 FCIVGWGPVAVVTI--ILTISPDNYGLSGYKRPNGSPDFCWINNN--AVFYI---TV 811

## RESULT 25

US-08-855-213-21  
; Sequence 21, Application US/08855213  
; Patent No. 5892004  
; GENERAL INFORMATION:  
; APPLICANT: ONDA, Haruo  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: KITADA, Chieko  
; APPLICANT: ISHIBASHI, Yoshihiro  
; APPLICANT: HOSoya, Masaki  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: MIYAMOTO, Yasunori  
; APPLICANT: HABATA, Yugo  
; APPLICANT: SHIMAMOTO, No. 5892004io  
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR  
; TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/855,213  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/202,986  
; FILING DATE: 25-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, David S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 44168  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 495 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-855-213-21

Db 268 YTIIGMTPTVCVTVMVAVRLYFDDAG-----CWMNDSTALWVVKGPV 312  
QY 812 VGFCVIFELLNVMFIVL-----VOLCRIKKKKOLGAQRKTSIQD 852  
Db 313 VGSIMVNFVLFIGIILVOKLQSPDMGNGNESSYFSCVQKCYC--KPOAQHSCMKME 370  
QY 853 LRSI-----AGLTFLGLITWG--FAFFAWGPNVNT--FMYLFAI-FNTLOGFFIFICYV- 902  
Db 371 LSTITLRLARSTILLIPLFGIHVTVFAFSPENVSKRERLVFELGLSGFQGVVAVLYCFL 430  
QY 903 ---AKENVKQWRRYLCGKRLRLAENSQWS-----KTATNGLKKQTVNQGVSSSSNLSQSS 955  
Db 431 NGEVQAEIKRKRWSW----KVNRYFTMDFKRHPBSLASSGVNGGTQLSTLSKSSQLRMS 486  
QY 956 S 956  
Db 487 S 487

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Query Match      4.38; Score 231; DB 2; Length 495;
Best Local Similarity 22.68; Pred. No. 3e-10;
Matches 95; Conservative 74; Mismatches 146; Indels 106; Gaps 20;

QY 596 LGRNGRGWSD-----NGCSVKDRRLNETICTGSHLTSFGVLLDLRTSVLPQAQMMAL 649
Db 113 VGRNCTEDGSEPPHYFDACGDDYE-----PESGDQDYYVLSV 152

QY 650 TTTYICGGLSSIFSLVTLVYIAFEKIR--RDYPSKILIQCAALLLNVLFLDLSWIA 707
Db 153 KALYTVGYSTSLATLTAMVILCRFKLCHTRNF---IHMNLFVSFMLRAISVFIKDWI- 208

QY 708 LYKMOGL-----CISVAVELHYFLVSTWGLCAFHMVLAIVKVENTYIRKYILK 758
Db 209 LYAEQDSSHCFVSTVECKAVWFFHYCVVSNFWLFIIEGLYFTLLVETFEFPE-RRIFYW 267

QY 759 FCIVGWGPVAVVVTI--ILTISPONYGSGYKFPNGSPDDEFCWNNNN--AVFYI---TV 811
Db 268 YTIIGWGTPTVCVTWAVLRLYFDDAG-----CWDMDNSTALWVVIKGPV 312

QY 812 VGYFCVIFLLNVSMFIVVL-----VOLCRKKKKQLGAQRKTSIQD 852
Db 313 VGSIMVNFVLFIGIIILVQKLQSPDMGNGNESSIYFSCVKCYC--KQRAQQHSCMKSE 370

QY 853 LRSI---AGLTFLGLITWG--FAFFANGPVNVT--FMVLFAT-FNTLOGFFIFIFYCV- 902
Db 371 LSTITLRLARSTLLIPLFGIHYTVAFSPENVSKRERLVFELGLSGFQGFVVAVLYCFL 430

QY 903 ---AKENVKOWRRYLCGKRLRLAENSQMS-----KTATNGLKKQTVNQGVSSSSNSLOSS 955
Db 431 NSEVOAEIKRKRSW---KVNRYFTMDFKHRHPSLASSGVNGGTQLSILSKSSQLRMS 486

QY 956 S 956
Db 487 S 487

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Search completed: May 23, 2002, 07:38:04  
Job time: 164 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2002, 07:36:21 ; Search time 25.95 Seconds  
(without alignments)  
3843.573 Million cell updates/sec

Title: US-09-731-657-2

Perfect score: 5352

Sequence: 1 SQPEDASGRCAQRFSTLFE.....GRMALRRTSKRSLHFIEQM 1038

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	536.5	10.0	1283	2	T18394 latrophilin-3, spl
2	536.5	10.0	1351	2	T18409 latrophilin-3, spl
3	536.5	10.0	1512	2	T18392 latrophilin-3, spl
4	536.5	10.0	1580	2	T18407 latrophilin-3, spl
5	536	10.0	1459	2	T17186 CL3AA protein - ra
6	536	10.0	1527	2	T17198 CL3BA protein - ra
7	534	10.0	1274	2	T18391 latrophilin-3, spl
8	534	10.0	1342	2	T18405 latrophilin-3, spl
9	534	10.0	1450	2	T18382 latrophilin-3, spl
10	534	10.0	1503	2	T18389 latrophilin-3, spl
11	534	10.0	1571	2	T18395 latrophilin-3, spl
12	533.5	10.0	1240	2	T18393 latrophilin-3, spl
13	533.5	10.0	1308	2	T18408 latrophilin-3, spl
14	532	9.9	1273	2	T17188 CL3AC protein - ra
15	532	9.9	1341	2	T17200 CL3BC protein - ra
16	531.5	9.9	1407	2	T18381 latrophilin-2 (spl)
17	531.5	9.9	1550	2	T14327 alpha-latrophilin r
18	531	9.9	1231	2	T18390 latrophilin-3, spl
19	531	9.9	1299	2	T18398 latrophilin-3, spl
20	528.5	9.9	1465	2	T18384 latrophilin-2 (spl)
21	527.5	9.9	1453	2	T18386 latrophilin-2 (spl)
22	526	9.8	1422	2	T18383 latrophilin-2, spl
23	525	9.8	1230	2	T17187 CL3AB protein - ra
24	525	9.8	1298	2	T17199 CL3BB protein - ra
25	525	9.8	1420	2	T18385 latrophilin-2 (spl)
26	522	9.8	1478	2	T18388 latrophilin-2 (spl)
27	520.5	9.7	1384	2	T18366 latrophilin-2, spl
28	519.5	9.7	1435	2	T18387 latrophilin-2, spl
29	518	9.7	1341	2	T18301 latrophilin-2, spl

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latrophilin-2 (spl  
latrophilin-2 (spl  
latrophilin-2 (spl  
CL1AA protein - ra  
CL1BA protein - ra  
latrophilin-2 (spl  
latrophilin-2 (spl  
CL2AC protein - ra  
latrophilin-1, bra  
CL2AB protein - ra  
CL2BC protein - ra  
alpha-latrophilin r  
CL2BB protein - ra  
CL2AA protein - ra  
CL1AB protein - ra  
CL1BB protein - ra  
CL2BA protein - ra  
leucocyte antigen  
seven-pass transme  
hypothetical prote  
probable hormone r  
brain-specific ang  
brain-specific ang  
MSGF2 protein - nu  
brain-specific ang  
hypothetical prote  
pituitary adenylat  
pituitary adenylat  
corticotropin-rele  
pituitary adenylat  
pituitary adenylat  
vasoactive intesi  
pituitary adenylat  
pituitary adenylat  
corticotropin rele  
corticoliberin rec  
corticotropin-rele  
vasoactive intesti  
vasoactive intesti  
CAR receptor - mou  
secretin receptor  
corticoliberin rec  
suvagine/corticot  
glucagon-like pept  
calcitonin-like re  
protein CL3B9.4 [i  
hypothetical prote  
calcitonin recepto  
PACAP/VIP receptor  
glucagon-like pept  
parathyroid hormon  
secretin receptor  
parathyroid hormon  
calcitonin recepto  
calcitonin recepto  
parathyroid hormon  
glucagon-like pept  
probable membrane  
parathyroid hormon  
parathyroid hormon  
hypothetical prote  
hypothetical prote  
calcitonin recepto  
calcitonin recepto  
vasoactive intesti

ALIGNMENTS

RESULT 1	
Tl8394	
latrophilin-3, splice variant abbb, brain-specific - bovine	
C:Species: Bos primigenius taurus (cattle)	
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000	
C:Accession: Tl8394	
R:Matsumita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.	
FEBS Lett. 443, 348-352, 1999	
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with diiffe	
A:Reference number: Z18869; MUID:99148828	
A:Accession: Tl8394	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-1283 <MAT>	
A:Cross-references: EMBL:AF111090; NID:g4164062; PID:g4164063; PIDN:AAD05326.1	
C:Superfamily: alpha-latotoxin receptor, calcium-independent	
C:Keywords: alternative splicing; G protein-coupled receptor	
Query Match 10.0%; Score 536.5; DB 2; Length 1283;	
Best Local Similarity 23.7%; Pred. No. 3.9e-23;	
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;	
QY 260 LQPIVCLADHPRGPPFSSSSQSIPIVPRATVLSQVPKATSFAPEDPDYSPVTHNVPSPIGE 319	
DB 409 ISPIHLDSDLERPVREISTGTGCTGTTTTLRTTT-----WSPGRSTTPSVSGR 462	
QY 320 IQPLSPQSPAPIASSPAIDMPQSETISSPMPQTHVSGTPPPVKASFSS----- 368	
DB 463 RNRSTSTP-----SPAIEVLNDI-----THVPSASPOIPALEESCEAVEAREIMW 508	
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVLOMEKALS 410	
DB 509 FKTRQGOMAKQPCPAGTIGVSTYLCLAPDGIWDPQGDLSNCS--SPWNHITOKLKS-- 564	
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440	
DB 565 -GETAANTARELAEQTRNHLNAGDITYSVRAMQDLVGLLDVQLRNLTPGKDSAAARSLNK 623	
QY 441 -----AQRLLKVVDDIGLQNFNS-----TTISLTSPSLALAVIR-----VNAS 479	
DB 624 LQKRESCRAYQAVETVNNL-LQPOLNARWDLTSDQLRAATMLLDTVESAFVLAD 682	
QY 480 SFNTTFFVAQDPANLQVLETOAPENSIGTITLPSL-----MNNLPAHDMELASR 530	
DB 683 NLLKTDIVRENTDNIQLEVARLSTEGNLDLKFPENTGHGTTIQLSANTLKQNGRGEIR 742	
QY 531 VQFNFFET--PALFQDPSPLENLSL-----ISYVISSSVANLTVRN-----LTR 571	
DB 743 VAFVLYNNLGPYL-----STENASMKLGTTEAMSTNHSVIVNSPVITAANKFESNKVYLAD 798	
QY 572 NVTVLKHNPSODELTVCVFDWDLGRNGRGWSNGCSVKDRRLNETICTCSHLTSFG 631	
DB 799 PVVFTVKHIKQSEENFNPCSEFWSYKRTMTGYWSTQGCRLTTNKTHTTCCSNHLTNFA 858	
QY 632 VLL-----DLRSTSVLPQAOMMALTFITVIGCGLSIFLSVTLVTYIAFEKIRRDYPSKILIQ 688	
DB 859 VLMAHVEKHSADV--HDLLDVITWVGILLSVCLLICITFCFFRGLQSD--RNTIHK 915	
QY 689 LCAALLLNLFLL-----DSWIALYKMGCLCSIVAFVLFYLLVSTWGLFAFHYLA 743	
DB 916 LCISLFAELLFLIGINRDTQPIA-----CAVFAALLHFFFLAFTWFMLEGVQVLIY 968	
QY 744 LKVPNT--YIRKYILKFCVIGWGPVAVVVTIILTISPDNYGLGSYKFPNGSPDDFCWI 801	
DB 969 LVEFESEHSRKY---FVLVGYGMPALIVAVSAADYRSYG-----TDKVCWL 1014	
QY 802 NNNAVFYITVVGFCVIFLLNYSMTFVVLVOLGRICK--KKQLGAQRKTSIQDLR----- 854	
DB 1015 RLDTYFIWSFIGPATLIIMNLVIFLGIALYKMFHHTAILKPESCCLDNINYEDNRPFILKS 1074	

RESULT 2	
Tl8409	
latrophilin-3, splice variant bbbh, brain-specific - bovine	
C:Species: Bos primigenius taurus (cattle)	
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000	
C:Accession: Tl8409	
R:Matsumita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.	
FEBS Lett. 443, 348-352, 1999	
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di	
A:Reference number: Z18869; MUID:99148828	
A:Accession: Tl8409	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-1351 <MAT>	
A:Cross-references: EMBL:AF111096; NID:g4164074; PID:g4164075; PIDN:AAD05332.1	
C:Superfamily: alpha-latotoxin receptor, calcium-independent	
C:Keywords: alternative splicing; G protein-coupled receptor	
Query Match 10.0%; Score 536.5; DB 2; Length 1351;	
Best Local Similarity 23.7%; Pred. No. 4.2e-23;	
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;	
QY 260 LQPIVCLADHPRGPPFSSSSQSIPIVPRATVLSQVPKATSFAPEDPDYSPVTHNVPSPIGE 319	
DB 477 ISPPHLDSDLERPVREISTGTGCTGTTTTLRTTT-----WSPGRSTTPSVSGR 530	
QY 320 IQPLSPQSPAPIASSPAIDMPQSETISSPMPQTHVSGTPPPVKASFSS----- 368	
DB 531 RNRSTSTP-----SPAIEVLNDI-----THVPSASPOIPALEESCEAVEAREIMW 576	
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVLOMEKALS 410	
DB 577 FKTRQGOMAKQPCPAGTIGVSTYLCLAPDGIWDPQGDLSNCS--SPWNHITOKLKS-- 632	
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440	
DB 633 -GETAANTARELAEQTRNHLNAGDITYSVRAMQDLVGLLDVQLRNLTPGKDSAAARSLNK 691	
QY 441 -----AQRLLKVVDDIGLQNFNS-----TTISLTSPSLALAVIR-----VNAS 479	
DB 692 LQKRESCRAYQAVETVNNL-LQPOLNARWDLTSDQLRAATMLLDTVESAFVLAD 750	
QY 480 SFNTTFFVAQDPANLQVLETOAPENSIGTITLPSL-----MNNLPAHDMELASR 530	
DB 751 NLLKTDIVRENTDNIQLEVARLSTEGNLDLKFPENTGHGTTIQLSANTLKQNGRGEIR 810	
QY 531 VQFNFFET--PALFQDPSPLENLSL-----ISYVISSSVANLTVRN-----LTR 571	
DB 811 VAFVLYNNLGPYL-----STENASMKLGTTEAMSTNHSVIVNSPVITAANKFESNKVYLAD 866	
QY 572 NVTVLKHNPSODELTVCVFDWDLGRNGRGWSNGCSVKDRRLNETICTCSHLTSFG 631	
DB 867 PVVFTVKHIKQSEENFNPCSEFWSYKRTMTGYWSTQGCRLTTNKTHTTCCSNHLTNFA 926	
QY 632 VLL-----DLRSTSVLPQAOMMALTFITVIGCGLSIFLSVTLVTYIAFEKIRRDYPSKILIQ 688	
DB 927 VLMAHVEKHSADV--HDLLDVITWVGILLSVCLLICITFCFFRGLQSD--RNTIHK 983	

QY 689 LCAALLLLNLVFL-----DSWIALYKMGCLISVAVFLHYFLVSVFTWMGLEAFHMYLA 743  
Db 984 LCISLFAELLFLIGINRTDPIA-----CAVFAALLHFFFLAAFTWMFLEGVQLYIM 1036  
QY 744 LKVENT--YIRKYLKFCVGVPAVVVILLISPDNYGLSGYKGPNGSPDDFCWI 801  
Db 1037 LVEVFESHSRRY---FYLVGYGMPALIVAVSAADYRSYG-----TDKVCWL 1082  
QY 802 NNNAVFIYTVGVFCVFLNVMFIVVLVOLCRICK--KKOLGAQRKTSIODLR----- 854  
Db 1083 RLDTYFIWFIGPATLIIMLVIFLGIALYKMFHHTAILKPESGCLDNTYEDNRPFIKS 1142  
QY 855 ---SIAGLFLGITWGFAPFAGVNVVTFMYLFAFNLTQGFIFFYCYVAKENVRKOW 911  
Db 1143 WVGATALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFHCVLQKKVKEY 1202  
QY 912 RRYL---CC-----GKRLAENDSWKSTATNGLKKQVNOGVSSS 948  
Db 1203 GKCLRTHCCSGRSTESSIGSKTSGRTPGYSQSRIRRMWMDTVRKQSESSFITGD 1262  
QY 949 SNSLOSSNSTNTLLVNNDCSVHASGN 977  
Db 1263 INSSASLRNGAMHLLISNALLRPHGTNN 1291  
RESULT 3  
T18392  
latrophilin-3, splice variant abbf, brain-specific - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T18392  
R:Matsushita, H.; Lellanova, V.G.; Ushkaryov, Y.A.  
FEBS Lett. 443, 348-352, 1999  
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with diffe  
A:Reference number: Z18869; MUID:99148828  
A:Accession: T18392  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1512 <MAT>  
A:Cross-references: EMBL:AF111088; NID:94164058; PID:94164059; PIDN:AAD05324.1  
C:Superfamily: alpha-latrototoxin receptor, calcium-independent  
C:Keywords: alternative splicing; G protein-coupled receptor  
Query Match 10.0%; Score 536.5; DB 2; Length 1512;  
Best Local Similarity 23.7%; Pred. No. 4.9e-23;  
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;  
QY 260 LQDPIVLADHPGPPFSSSOSIPVVPVPRATVLSQVPKATSAEPDPYSPVTHNVPSPIGE 319  
Db 409 ISPPHLDSDLRPPVREISTGTPLGTGTTTTLRTT-----WSPGRSTTSPVSGR 462  
QY 320 IQLSPQPSAPITASSPAIDMPPQSETISSPMQTHVSGTPPVPKASFS----- 368  
Db 463 RNRSTP-----SPAIEVLNDI-----THVPSASQIPALEESCEAVEAREIMW 508  
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVLEKALS 410  
Db 509 FKTRQGMQKPCPAGTIGVSTYLCLAPDGIWDPQDLSNCS--SPWVNHTQKLKS-- 564  
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440  
Db 565 -GETAANIARELAETRNHLNAGDITYSVRAMQVLGLDVLQRLNLTTPGKDSAAARSLNK 623  
QY 441 -----AQRLLKVDDIGLQNFN-----TTISLTSPSLALAVTR-----VNAS 479  
Db 624 LQKRERSCRAYVOAMVETVNNL-LQPOLANAWRLDTTSDQLRATMLLDTVEESAFVLAD 682  
QY 480 SFNFTTFAQADPANLQVSLQETQAPENSIGFITLPSSL-----MNNLPAHIDELASR 530  
Db 683 NLLKTDIVRENTDNTQLEVARLSTEGNLEDKFPENFGHGSTIQLSANTLKONGRNGEIR 742  
QY 531 VQNFET--PALFQDPSLENLSL-----ISYVISSSVANLATVRN-----LTR 571

Db 743 VAFVLNNLGPYL-----STENASMKLGTMTNSTHSVIVNSPVITTAINKFSGNKVYLAD 798  
QY 572 NVTVTLLKHINPSODELTVRCVFDLGRNGRGWSDNGSVKDRRLNETICTCGSHITSFG 631  
Db 799 PVVFTVKHIQSEENFNENFNCPSFWSYSKRTMTGYWSTQGCRLTTNKTHTTSCNHLNFA 858  
QY 632 VLL---DLSTSVLPAQMMALTFITYICGGLSSIFSLSVTLVITYIAFEKIRRDYPSKILIQ 688  
Db 859 VLMHAEVKHSDAV--HDLILLDVITWVGILLSVCLLCIFTCFGRGLQSD-RNTIHN 915  
QY 689 LCAALLLLNLVFL-----DSWIALYKMGCLISVAVFLHYFLVSVFTWMGLEAFHMYLA 743  
Db 916 LCISLFAELLFLIGINRTDPIA-----CAVFAALLHFFFLAAFTWMFLEGVQLYIM 968  
QY 744 LKVENT--YIRKYLKFCVGVPAVVVILLISPDNYGLSGYKGPNGSPDDFCWI 801  
Db 969 LVEVFESHSRRY---FYLVGYGMPALIVAVSAADYRSYG-----TDKVCWL 1014  
QY 802 NNNAVFIYTVGVFCVFLNVMFIVVLVOLCRICK--KKOLGAQRKTSIODLR----- 854  
Db 1015 RLDTYFIWFIGPATLIIMLVIFLGIALYKMFHHTAILKPESGCLDNTYEDNRPFIKS 1074  
QY 855 ---SIAGLFLGITWGFAPFAGVNVVTFMYLFAFNLTQGFIFFYCYVAKENVRKOW 911  
Db 1075 WVGATALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFHCVLQKKVKEY 1134  
QY 912 RRYL---CC-----GKRLAENDSWKSTATNGLKKQVNOGVSSS 948  
Db 1135 GKCLRTHCCSGRSTESSIGSKTSGRTPGYSQSRIRRMWMDTVRKQSESSFITGD 1194  
QY 949 SNSLOSSNSTNTLLVNNDCSVHASGN 977  
Db 1195 INSSASLRNGAMHLLISNALLRPHGTNN 1223  
RESULT 4  
T18407  
latrophilin-3, splice variant bbbf, brain-specific - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T18407  
R:Matsushita, H.; Lellanova, V.G.; Ushkaryov, Y.A.  
FEBS Lett. 443, 348-352, 1999  
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di  
A:Reference number: Z18869; MUID:99148828  
A:Accession: T18407  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1580 <MAT>  
A:Cross-references: EMBL:AF111094; NID:94164070; PID:94164071; PIDN:AAD05330.1  
C:Superfamily: alpha-latrototoxin receptor, calcium-independent  
C:Keywords: alternative splicing; G protein-coupled receptor  
Query Match 10.0%; Score 536.5; DB 2; Length 1580;  
Best Local Similarity 23.7%; Pred. No. 5.2e-23;  
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;  
QY 260 LQDPIVLADHPGPPFSSSOSIPVVPVPRATVLSQVPKATSAEPDPYSPVTHNVPSPIGE 319  
Db 477 ISPPHLDSDLRPPVREISTGTPLGTGTTTTLRTT-----WSPGRSTTSPVSGR 530  
QY 320 IQLSPQPSAPITASSPAIDMPPQSETISSPMQTHVSGTPPVPKASFS----- 368  
Db 531 RNRSTP-----SPAIEVLNDI-----THVPSASQIPALEESCEAVEAREIMW 576  
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVLEKALS 410  
Db 577 FKTRQGMQKPCPAGTIGVSTYLCLAPDGIWDPQDLSNCS--SPWVNHTQKLKS-- 632  
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440

Db	633	-GETAANIARELAQTRNHLNAGDITYSVRAMDQVLGLDVLQRLNLTGGKDSAARSLNK	691
Qy	441	-----AQRLLKVVDDIGLQNFN-----TTISLTSPSLALAVIR-----VNAS	479
Db	692	LQKRERSCRAYVOAMVETVNNL-LQOQALNAWRDLTTSQDLRAATMLDVTVEESAFVLAD	750
Qy	480	SNFTTTFVAQDPANLQVSLAQAPENSIGTITLPSSL-----MNNLPAHDMELASR	530
Db	751	NLTKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKONGRNGEIR	810
Qy	531	VQNFET--PALFQDPSLENLSL-----ISYVSSSVANLTVRN-----LTR	571
Db	811	VAFVLYNNLGPYL-----STENASMKLGTTEAMSTNHSVINSPVITAAINKFESKVVY	866
Qy	572	NVTTLKHINPSQDELTVRCVFDLGRNGRGWGSDGSKVDRRLNETICTCSHLTSEF	631
Db	867	PVFTVKHIQKQSEENFNPCSFWSYKRTMTGYWSTQGCRLTTNKTHTTCSNHLTNEA	926
Qy	632	VLL---DLRSTSVLPAOMMALTFITYICGLSSIFLSVTLVTYIAFEKIRRDYPSKILIQ	688
Db	927	VMAHVEVKHSDAV--HDLLEDVITWVGILLSLVCLLCIIFTCFFRGLOSD-RNTHKN	983
Qy	689	LCRAALLNLNLFLL-----DSWIALYKMQGLCISVAVFLHYFLYLLVFTWMGLEAFHMYLA	743
Db	984	LCISLFAELLFLIGINRTDQPIA-----CAVFAALLHFFFLAAFTWMLEGVQLYIM	1036
Qy	744	LVKVFT--YTRKYLKFCIVGWGPVAVVITILLISPDNYGLSGKFPNGSPDDFCWI	801
Db	1037	LVEFESEHSRKY---FYLVGYGMPALIVAVSAAVDYRSYG-----TDKVCWL	1082
Qy	802	NNNAVEYTVVGYFCVIFLLNVSMFIVLVQLCRIKK--KKOLGAQRKTSIQDLR-----	854
Db	1083	RLDIYFTWSFGPATLIIMNLNVLFGIALYKMFHTAILKPESGCLDNIYEDNRPEIKS	1142
Qy	855	---SIAGTLFLGLTGWGPAFWGPNVTVMYLFALNTLQGFIFIPYCVAKENVRKQW	911
Db	1143	AVIGAIALLCLGLTWAFGLMYINESTVMAYLFTIFNSLQGMFIFPHCVLQKVRKEY	1202
Qy	912	RYL---CC-----GKURLAENSQWSTATNGLKKOTVNOGVSSS	948
Db	1203	GKURTHCCSRSTESSIGSKTSRTPGRYSTGSQSRIRRMWNTVTRKQSESSFITGD	1262
Qy	949	SNLSQSSNSTNTLLVNNDCSVHASGN	977
Db	1263	INSSASLNRGAMANHLISNALLRPHGTNN	1291
RESULT	5		
CL3BA	protein - rat		
C:	Species: Rattus norvegicus (Norway rat)		
C:	Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000		
C:	Accession: T17186		
R:	Sugita, S.; Ichchenko, K.; Khvotchev, M.; Sudhof, T.C.		
A:	submitted to the EMBL Data Library, July 1998		
A:	Description: CL family.		
A:	Reference number: 218712		
A:	Accession: T17186		
A:	Status: preliminary; translated from GB/EMBL/DBJ		
A:	Molecule type: mRNA		
A:	Residues: 1-1459 <SUG>		
A:	Cross-references: EMBL:AF081154; NID:g3695134; PID:g3695135; PIDN:AAC62660.1		
C:	Superfamily: alpha-latrototoxin receptor, calcium-independent		
Query Match	10.0%	Score	536;
Best Local Similarity	24.7%	Pred. No.	5e-23;
Matches	218;	Conservative	131;
		Mismatches	344;
		Indels	190;
		Gaps	35;
Qy	248	SSPELGLQLQCDLQDPIVGLADHPGRPFSSQSIQVVPVPRATVLSQVVKATSFAPPDYS	307
Db	398	SGPVHGVQVSY-ISPPHILDSDLRPPVPGVISTGTLGMSGTTTSTTLRTTNLGRSTT	456

R:Matsushita, H.; Lelianova, V.G.; Ushkaryov, Y.A.  
FEBS Lett. 443, 348-352, 1999  
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di  
A:Reference number: Z18869, MUID:99148828  
A:Accession: T18391  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1274 <MAT>  
A:Cross-references: EMBL:AF111087; NID:q4164056; PID:q4164057; PIDN:AAD05323.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent  
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match	10.0%	Score 536;	DB 2;	Length 1527;
Best Local Similarity	24.7%;	Pred.	No. 5.3e-23;	
Matches 218;	Conservative 131;	Mismatches 344;	Indels 190;	Gaps 35;
QY	248	SSPEELGKLOCDLQDPIVCLADHPRGPPFSSSQSIPVVPRAIVLSQVPKATSPAEPDYS	307	
DB	466	SGPVHGVSY-ISPPIHLDSDLERPVRGISTGPGMGSTTTTTLTTTWNLGRSTT	524	
QY	308	PV-----THNVSPSIGEIQPLSPSPASPIASSPAIDMPQSEISSPMPQTHVSGTTP	360	
DB	525	PSLPGRRNRSTSPS-AIEVLDVTHLPSAASQIPAMEESCEAVEAIEWMFKTRQG	582	
QY	361	PVKASFSEPTVS-----APANVNTSAPVQTDIVNTSISDLNQVLOMEKALSLS	413	
DB	583	VAKOSCPAGTIGVSTYLCIAPDGDWDPQG-----DLSNCS--SPWVNHTOKLKS--GE	633	
QY	414	LEPNLAGMINQVSRLLHS-----PPDMLAPL-----	440	
DB	634	TAMIAELAEQTRNHLNAGDITYSVRAMDOLVGLLDVOLRLN/TPGGKDSAAARSLNKLQK	693	
QY	441	-----AORLLKVVDDIGLQLNFEN-----TTISLTSPLALAVIR-----VNASSFN	482	
DB	694	RESCRAYQAWVETVNNL-LOQALNAPFDLTSQDLRAATMLDVTVEESAFVILADNLL	752	
QY	483	TTTFEVAQDANLOVSLAQAPENSIGITILPSSL-----MNNLPAHDMELASRVQF	533	
DB	753	KTDIVRENTNIOLEVARLSTEGNLEDLAKFPENTGHGSTIQLSANTLQKNGRGEIRVAF	812	
QY	534	NFFET--PALFQDPSLENLSL-----ISYVISSSVANLAVRN-----LTRNVT	574	
DB	813	VLNNLGPYL-----STENASKMLGTETAMSTNHVSNVSPVITAAINKEFSNKVYLADPVV	868	
QY	575	VTLLKHINPSODELAVRCVFDWLGRRNGRGWSGSCVKDRRLNETICTCSHLTSFGVLL	634	
DB	869	FTVKHKIQSEENFNPCSFWSYKRTMTGYWSTQGCRLLTNKTKTTCSCNHLTFEAVLM	928	
QY	635	---DLSTSVLPQAOMMALTFITYIGGLSISFLSVLTVTYIAFEKIRRDYPSKILIQCA	691	
DB	929	AHVEVKHSDAV--HDLLLDVITWVGILLVLCILICITFCFFRGLQSD-RNTIHKNLCI	985	
QY	692	ALLLLNLVFL-----DSWIALYKMOGLCISAVELHYFLVLSFTWMCLEAFHMYLALVK	746	
DB	986	SLFVAELFLIGINRTDQPIA-----CAVFAALLHFFFAAFTWFEGLVQLYIMLVE	1038	
QY	747	VFNT--YIRKYILKFCIVGWGPVAVVVTIILTISPQNYGLSGYKPNGPSDDFCWNNN	804	
DB	1039	VFESHSRRRY--FYLVGYGMPALIVAVSAADVRSYG-----DVKVCWLRLD	1084	
QY	805	AVFYITVGVGFCVFLNLVSMFIVVLVOLCRKK--KKQLGAQRKTSIQDRIISAGLTFL	862	
DB	1085	TYFIWFGPATLIILNIFGLIAYKMFHTAILKPESGCLDNIKSWVIGALIA-LLCL	1143	
QY	863	LGITGFAFFAWGPVNTFMYLFAFNLTLOGGFIFIFYCVAKENVRKQW-----RRLCCG	918	
DB	1144	LGLTWAGFLMYINESTVIMAYLFIIFNSLOGMFIFIFHCVLQKVRKEYGKCLTHCCSG	1203	
QY	919	KL-----RLAENSD-----WSKATATNGKKQTVNQGVSSSSNSLQSS	955	
DB	1204	KSTESSIGSKTSGSRTPGRYSTGQSRIIRMWNDT---VRQSESSFTIGDIN---S	1255	
QY	956	SNSTNSTTLLVN-NDCSVHAS--GNGNASTERNGVSVFVONGD	995	
DB	1256	SASLNREGLLNNAADTSVMDTPLNNG-----HGNSYSTAGGE	1293	

```
RESULT 7
T18391
catophilin-3, splice variant abah, brain-specific - bovine
;;Species: Bos primigenius taurus (cattle)
;;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
;;Accession: T18391
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QY 957 NSTNSTLLVNDSCSVHASN 977  
Db 1194 RGAMANHLISNALLRPHGTNN 1214  
RESULT 8  
T18405  
latrophilin-3, splice variant bbah, brain-specific - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T18405  
R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.  
FEBS Lett. 443, 348-352, 1999  
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with different functions  
A:Reference number: Z18869; MUID:99148828  
A:Accession: T18405  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1342 <MAT>  
A:Cross-references: EMBL:AF111093; NID:g4164068; PID:g4164069; PIDN:AA05329.1  
C:Superfamily: alpha-latrototoxin receptor, calcium-independent

Query Match 10.0%; Score 534; DB 2; Length 1342;  
Best Local Similarity 23.9%; Pred. No. 5.8e-23;  
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;

QY 260 LQPIVCLADHGRPPSSSOSIPVPRATVLSQVQKATSAEPDPYSPVTHNVSPICE 319  
Db 477 ISPIHLDSLRPPVREISITGLTGSTTTTLRTT-----WSPGRSTTPSVSGR 530  
QY 320 IQPLSPQSAPIASSPAIDMPQSETISSPMQTHVSGTPPPVKASFSS----- 368  
Db 531 RNRSTSTP-----SPAELVNDI-----THVPASQIIPALEESCEAVEAREIMW 576  
QY 369 -----PTVSAPANVT-----TSAP-----PVQTDIVNTSSIDLENQVLMKEKALS 410  
Db 577 FKTRQGMQKQPCFAGTIGVSTYLCAPDGIWDQPGDLSNCS--SPWVNHTQKLKS-- 632  
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440  
Db 633 -GETAANIARELAEOIRHNLNAGDITYSVRAMDQVGLDVLQRLNTPCGKDSAAKSLNK 691  
QY 441 -----AQRLLKVVDDIGLQNFN-----TTISLTPSLALAVIR-----VNAS 479  
Db 692 LQKRSRCRAYQAMVETVNNL-LQPALNAWRDLTSDQLRAATMLLDTVEESAFVLAD 750  
QY 480 SFNTTTFVAQDPANLQVSLQAPENSIGTITLPSL-----MNNLPADHMLASR 530  
Db 751 NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFEPENTGHGSIQLSANTLKONGRNGEIR 810  
QY 531 VQNFEEF--PALQDPDSLENLSL-----ISYVSSSVANLTVRN-----LTR 571  
Db 811 VAFVLYNNLGPYL-----STENASKMLGTEAMSTNHSIVNSPVITAANKFESKVLAD 866  
QY 572 NVTVTLKHINPQDELATVRCVFDLGRNGRGWGSDNGSVKDRRLNERICTCSHLTSFG 631  
Db 867 PVVTVKHQKSEENFNPCSFWSYKRTMTGYSTQGCGRLLTNTKTHTCSCNHLTNFA 926  
QY 632 VLL---DLRSTSVLPQAMMALTFITYIGGLSSIFLSVTLVTVIAFEKIRRDYPSKILIQ 688  
Db 927 VLMAHVEKHSADAV--HDLLELVITWVGILLSLVLCILICIFTCFGRGLQSD--RNIHKN 983  
QY 689 LCAALLNLNLVFL-----DSWIALYKMGCLGISVAVFLHYFLVLSFTWMGLEAFHMYLA 743  
Db 984 LCISLFAELLFLGINRTDQIA-----CAVFAALLHFFFLAFTWMELEGVQLYIM 1036  
QY 744 LVKVFNT--YIRKYILKFCIVGWGPVAVVVVITLITSPDNYGLSGKFGPSPDPCFWI 801  
Db 1037 LVEVFESEHSRRKY---FVLVGYGMPALIVAVSAAYDIRSYG-----TDKVCWL 1082  
QY 802 NNAVFYITVVGFCVIFLLNYSMEFIVLVQLCRICK--KKQLGAQRKTSIQDLRSLAGL 859

Db 1083 RLDTYFIWSFIGPATLIIMLVNFIAGIALYKMFHHTAILKPSGCLDNKSKSVVGAIA-L 1141  
QY 860 TFLGLGTWGAFAFWGPNVNTFMVLFALFNTLQGFIEFYCVAKENVRKOWRRYL--C 916  
Db 1142 LCLGLTWAEGLYINVESTYIMAYLTFIENSLQGMFIFHCVLQKKVRKEYGKCLRTHC 1201  
QY 917 C-----GKURLAENSWSKATATNGLAKKQTVNQVQSSSSNSLQSSS 956  
Db 1202 CSGRSTESSICSGKTSRTPGRVSTGSRIRRMWMDTVRKQSESSFTIGDINSSASLN 1261  
QY 957 NSTNSTLLVNDSCSVHASN 977  
Db 1262 RGAMANHLISNALLRPHGTNN 1282  
RESULT 9  
T18382  
latrophilin-2 (splice variant bbaaf) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T18382  
R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.  
FEBS Lett. 443, 348-352, 1999  
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with different functions  
A:Reference number: Z18869; MUID:99148828  
A:Accession: T18382  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1450 <MAT>  
A:Cross-references: EMBL:AF111078; NID:g4164038; PID:g4164039; PIDN:AA05314.1  
C:Superfamily: alpha-latrototoxin receptor, calcium-independent  
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 10.0%; Score 534; DB 2; Length 1450;  
Best Local Similarity 23.3%; Pred. No. 6.5e-23;  
Matches 260; Conservative 168; Mismatches 455; Indels 234; Gaps 48;

QY 90 VETTSLND-----VTLSLLPSN-----ETEKTKITIVKTFNAGVKPQR 128  
Db 188 IEYASLEDFQNSRQTTTKYLPNRVDGTGVVYDGAFFNKRKTR-NIVKYDLTRIKSGE 246  
QY 129 NICNLSSICNDUSAFRG---ETMFQYDKES---TVPNQHOHITNGTLTGVLSSLSEKRS 180  
Db 247 ALIINYANTVHTDTPYRWGKGTDLDAVDENGLWVIYATEQN-----NGMIVLSQNPY 298  
QY 181 ELNKTQLTSETYFIMCATAEAQSTLCTFTKL-----NNTMNACAAIALERVKIRPME 236  
Db 299 TLR--FEATWETVDYKRAASNAFMICGVLYVRSVYQDNESGTCKNAIDYIYNRLNRGE 356  
QY 237 HCCSVRIPCSPSSPEELGKLCQDLPVCLADH-----PRGPP-----FS 277  
Db 357 Y---VDVFPFQYQYIAADVNDYPRDNQLYVNNNNFILRYSLEFGPPDPAQVPTAVTIT 412  
QY 278 SSQSI---PVVPRATVLSQVPKATSPA-----EPPDYSPVTHNVSPICEIQPLS 324  
Db 413 SSAEMFKTVTSITTSOKGPMSTTVAGSGEGSKGTAPPAVS--TTKIP--PVTNIEPL- 468  
QY 325 POPSAPIASSPAIDMP-----POSE---TSSPMQTHVSGTPPPVKASFSPPTVAPANV 377  
Db 469 -----PERFCEALDARGIRWPQTRGMVVERPCPK-----GT-----RGTASYLCVL 510  
QY 378 NTSAPPVQTDIVNTSS--ISDLENQVLMKEKALSIG-----SLEPNLAGEMINQVSR 429  
Db 511 STGTWNPKGPDLSNCTSHVWVNLQAQKIRSGENASLANELAKHTKGPVAGDVSSV-RL 569  
QY 430 LHSPPDML-APLAQRLLKVVDDIGLQIN--FSNTTISLTPSLALAVIRVNAS--SFNTTT 485  
Db 570 MEQLVDILDAQLELKPSEKDSAGRSYKNAIVDITVDNLLRPEALESWKHMNSSEQAHTAT 629  
QY 486 -----FVAODPANL---QVSLQETQ-----APENSIGTITLPSLMLN---- 518  
Db 630 MLDDTLEGAFLAD--NLVPEPTRVSMPTENIVLEAVLSTEGVQVQDFKFLGKAGSS 687

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QY 519 -NLPAHDMELASR---VQNFETFPALFQDPSLEN-----LSLSYVISS 559
D 688 IQLSANTVKQNSRGLAKLVFIYRSIGQFLSTENAIKLGADFIGRSTIAVNSHVLSV 747
QY 560 SVANLTVR-NLRTNVTTLKHINPSODELTVRCVFDLGRNGRGSGDNGSCVSKDRRLN 618
D 748 SINKESSRYLDPVLFPLPHIDP-DNYFNANGSFWNYSERTMGYWSQTGCKLVDTKT 806
QY 619 ETICTSHLTSGVLIDLSRTSVLP-AQMMALFTFIVIGGGLSIFLSVTLVYIAFEKI 677
D 807 RTTCACSHLTNFAILMAHREIAYKDGVEHLLVITWGVISLVCLAICTFCFFRGL 866
QY 678 RRDYPSKILIQCALLLNLVFLDLSWIALYKMQGLCISVAVFLHYFLVFTWMGLEA 737
D 867 QSD-RNTTHKLNLCINLFAERIFLIG-IDKTYMIACPIFAGLLHFFFLAAFAWMCLE 923
QY 738 FHYLALYKVENT-YIRKYLLKFCIVGWGPVAVVVTIILISPDNYGLSGYCKPNSGPD 796
D 924 VOLYLMLVEFESEYSRKY--YYVAGYLFPAATVGVSAADYKSYG-----TE 970
QY 797 DFCWINNNAVYITVVGFCVIFLLNVSMFIVLVQLCRKKKQOLGAQRKTSIQDLRS- 855
D 971 KACWLHDVNYFIWSPFGVTFIILLNI--IFLVITLCKMKVHSNTLKPDSRLNIKSW 1027
QY 856 IAG---LTFILGITWGAFFANGPVNVTWYLPFAINTLQGFIFIFCYVAKENVRKOW- 911
D 1028 VLGAFAALLGLTWISFGLLFINEETIVMAYLFTIFNAFGVFIIFHCALQKKVREYG 1087
QY 912 ---RRLYCCGKRLAENSWSKTAT-----NCLKQTVNQGVSS 948
D 1088 KCFRHSYCCGLPTESPSSVSKASTRTSARYSQGSRIRRMWMDTVRKQSESFISGD 1147
QY 949 SNSLQSSNSTNTLLVNDSCVHASGNGNASTERNGVSFQVQNGDVCLHDFGKOHMF 1008
D 1148 INSTSTLNOGMTGYLLNPLRLPBGHTNPNYNTLLAETVVCNAPSAPV----FNSPGHSL 1203
QY 1009 NEREDSC-----NCKGRMARLRTSKRGLHFT 1036
D 1204 NNARDTSAMDTLPLNGFNNSYLRKGDYNDVQVQVD 1240

RESULT 10
T18389
latrophilin-3, splice variant abaf, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18389
R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with different local similarity
A:Reference number: Z18869; MUID:99148828
A:Accession: T18389
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1503 <MAT>
A:Cross-references: EMBL:AF111085; NID:g4164052; PID:g4164053; PIDN:AAD05321.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 10.0%; Score 534; DB 2; Length 1503;
Best Local Similarity 23.9%; Pred. No. 6.8e-23;
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;

QY 260 IQDPIVLADHPGRPPFSQSIPVPRATVLSQVPKATSAEPDPYSPVTHNVPSPIGE 319
D 409 ISPPHILDSLDLPPVREISTGCLGTSTTTTLRTTT-----WSPGRSTTPSVSGR 462
QY 320 IQPLSPQPSAPIASSPAIDMPPQSETISSPMPQTHVSGTPPVPKASFSS----- 368
D 463 RNRSTSTP-----SPAIEVLNDI-----TTHVPSASPOIPALAESCEAVEAREIMW 508

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QY 369 -----PTVSAPANVNT--TSAP-----PVQTDIVNTSSISDLENQVLMKALS 410
D 509 FKTRQGMKQPCPAGTIGVSTYLCLAPDGTWDPQDLSNCS--SPWVNHTQKLKS-- 564
QY 411 LGSLEPNLAGEMINOVSRLLHS-----PPDMLAPL----- 440
D 565 -GETAANIAELAEQTRNHLNAGDIYSYRAMDQVLGLLDVQLRLNLTGGKDSAAARSLNK 623
QY 441 -----AQLKVVDDIGLQNFN-----TTISLTPSLALAVIR---VNAS 479
D 624 LOKRERSRAYVQAMVETVNNL--LOPALNAWRDLTTSQDLRAATMLLDTVEESAFVLAD 682
QY 480 SFNTTFVAQDPAQLQVLSLETOAPENSIGTITLPSLL-----MNNLPAHDMELASR 530
D 683 NLLKTDIVRENTDNLQLEVARLSTEGNLEDLKPENTGHSTIOLSANTLKONGRNGEIR 742
QY 531 YQNFET--PALFQDPSLENLSL-----ISYVSSSVANLTVRN-----LTR 571
D 743 VAFVLYNNLGPVL---STENASMKLGTTEAMSTNHSVIVNSPVITAAINKFESNKVYLAD 798
QY 572 NVTYTLKHINPSODELTVRCVFDLGRNGRGSGDNGSCVSKDRRLNETICTCSHLTSFG 631
D 799 PVFTVKHIKQSEENFNPNCSFWSYSKRTMTGYWSTQGCRLLTNTKTHTTCSCNHLTNFA 858
QY 632 VLL---DLSRTSVLPQAQMMALFTFIVIGCGLSIFLSVTLVYIAFEKIRRDYPSKILIQ 688
D 859 VLMAHVEVKHSDAV--HDLLLDVITWGLLSLVLLCICITFCFFRGLQSD-RNTIHK 915
QY 689 LCAALLLNVLFL-----DSWIALYKMQGLCISVAVFLHYFLVFTWMGLEAFHMYLA 743
D 916 LCISLFAELLFLIGINRTDQPIA-----CAVFAALLHFFFLAAFTWMLFEGVQIYIM 968
QY 744 LVKVENT--YIRKYLLKFCIVGWGPVAVVVTIILISPDNYGLSGYCKPNSGPDFOCI 801
D 969 LVEVFESEHSRKY---FYLVGMPALIVAVSAADVRSYG-----TDKVCWL 1014
QY 802 NNAVFYITVVGFCVIFLLNVSMFIVLVQLCRKK--KKOLGAQRKTSIQDLRSIAGL 859
D 1015 RLDTYFIWSPFGPATLIIMLVIFELGIALYKMFHFAILKPESCLDNKISWVIGAI-A-L 1073
QY 860 TFLGITWGAFFANGPVNVTWYLPFAINTLQGFIFIFCYVAKENVRKOWRYL---C 916
D 1074 LCLLGLTWAGFLYINESTVIMAYLFTIFNSLQGMIFIFHCVLQKKVREYGCRLRTHC 1133
QY 917 C-----GKRLAENSWSKTATNGLKQTVNQGVSSSSNSLQSS 956
D 1134 CSGRSTESSICSGKTSGRTPGRYSTGSRIRRMWMDIVRKQSESFITGDIINSSASLN 1193
QY 957 NSTNSTLLVNDSCVHASGN 977
D 1194 RGAMANHLISNALLRPHGTNN 1214

RESULT 11
T18395
latrophilin-3, splice variant bbaf, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18395
R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with different local similarity
A:Reference number: Z18869; MUID:99148828
A:Accession: T18395
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1571 <MAT>
A:Cross-references: EMBL:AF111091; NID:g4164064; PID:g4164065; PIDN:AAD05327.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 10.0%; Score 534; DB 2; Length 1571;

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A:Reference number: Z18869; MUID:99148828  
A:Accession: T18393  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1240 <MAT>  
A:Cross-references: EMBL:AF111089; NID:g4164060; PID:g4164061; PIDN:AAD05325.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent  
C:Keywords: alternative splicing; G protein-coupled receptor

Best Local Similarity 23.9%; Pred. No. 7.2e-23;  
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;  
QY 260 LODPTVCLADHPRGPPFSSOSIPVPRATVLSQVPKATSFAPEDPDYSPVTHNVPSPICE 319  
DB 477 ISPPHLDSDLERPPVREISTTGPLGTGTTTTLRTTT-----WSPGRSTTPSVSGR 530  
QY 320 IQPLSPQSPAPIASSPAIDMPPQSETISSPMQTHVSGTPPPVKASFSS----- 368  
DB 531 RNRSTSTP-----SPAIEVLNDI-----TTHVPSASPOIPALEESCEAVEAREIMW 576  
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSIDLENQVLMQEKALS 410  
DB 577 FKTRQGMAKQPCPAGTIGVSTYICLAPDGIWDQGPDLNCS--SPWVNHITQKLKS-- 632  
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440  
DB 633 -GETAANIAELAEQTRNLHLAGDITYSVRAMDQVLGLDVLRLNLTGPKDSDAARSLNK 691  
QY 441 -----AORLLKVDDIGLQNFN-----TTISLTSPSLALAVIR-----VNAS 479  
DB 692 LOKRERSCRAYQAMVETVNNL-LQOALNAWRDLTSDQLRAATMLDITVEESAFVLAD 750  
QY 480 SFNTTTFVAQDPANLQVSLQTPAPENSIGTITLPSL-----MNNLPAHDMELASR 530  
DB 751 NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPEPTGHGSTIQLSANTLKONGRNGEIR 810  
QY 531 VQNFPEET--PALFQDPSLENLSL-----ISYVSSSVANLTVRN-----LTR 571  
DB 811 VAPVLYNNLGPYL-----STENASMKLGTAMSTNHVSNVSPVITAAINKEFSNKVYLAD 866  
QY 572 NVTVTLKHNPSODELTVRVCFWDLGRNGRGSGDNGSVKDRRLNETICTCSHLTSFG 631  
DB 867 PVVFTVKHKKOSEENFNPCSFWSYKRTMTGYWSTQGCRLLTNNKTHTTCSNHLTNFA 926  
QY 632 VLL---DLSRTSVLPQAOMMALFTIYIGCGLSIFLSVTLVTVIAIEKIRRDYPSKILIQ 688  
DB 927 VLMAHVEVKHSDAV--HDLLEDVITWVGILLSVCLLCIETFCFFRGLQSD--RNTIHN 983  
QY 689 LCAALLLNLFLL-----DSWIALYKMOGLCISVAVFLHYFLVSVTWGMEAFHMYLA 743  
DB 984 LCISLFAELLELIGINRTDQPIA-----CAVFAALLHFFFLAAFTWMELEGVQLYIM 1036  
QY 744 LVKVFNT--YIRKYILKFCIVGWGPVAVVTVITLISPDNYGLSGYKFPNGSPDDFCWI 801  
DB 1037 LVEVESEHSRKY---FYLVGYGMPALIVAVSAADVRSYG-----TDKVCWL 1082  
QY 802 NNNAVFTYVVGFCVIFLLNVSMFIVLVOLCRICK--KKQLGAQRKTSIQDLRSIAGL 859  
DB 1083 RLDTYFIWISFGPATLIIMLVIFGLIYALYKMFHHTAILKPEGCLDNTKSVWIGALIA-L 1141  
QY 860 TFLGITWGAFFAWGPNVNTFMVLFALFNTLQGGFFIFIFYCVAKENVRKOWRYL---C 916  
DB 1142 LCLLGLTWAFGLMYNESTVIMAYLFTIENSLOGMFIFIFCHVLOKKVRKEYGKCLRTHC 1201  
QY 917 C-----GKRLAENSOWSKTATNGLKKQTVNOGVSSSSNSLOSSS 956  
DB 1202 CSGRSTESSIGSGTSGSRTPGRYSTGQSRIRRMWMDTVRKQSESSFITGIDINSSASLN 1261  
QY 957 NSTNSTLLVNNDCSVHASGN 977  
DB 1262 RGAMANHLISNALLRPHGTNN 1282

Query Match 10.0%; Score 533.5; DB 2; Length 1240;  
Best Local Similarity 24.2%; Pred. No. 5.6e-23;  
Matches 209; Conservative 123; Mismatches 345; Indels 187; Gaps 31;  
QY 260 LQDPIVCLADHPRGPPFSSOSIPVPRATVLSQVPKATSFAPEDPDYSPVTHNVPSPICE 319  
DB 409 ISPPHLDSDLERPPVREISTTGPLGTGTTTTLRTTT-----WSPGRSTTPSVSGR 462  
QY 320 IQPLSPQSPAPIASSPAIDMPPQSETISSPMQTHVSGTPPPVKASFSS----- 368  
DB 463 RNRSTSTP-----SPAIEVLNDI-----TTHVPSASPOIPALEESCEAVEAREIMW 508  
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSIDLENQVLMQEKALS 410  
DB 509 FKTRQGMAKQPCPAGTIGVSTYICLAPDGIWDQGPDLNCS--SPWVNHITQKLKS-- 564  
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440  
DB 565 -GETAANIAELAEQTRNLHLAGDITYSVRAMDQVLGLDVLRLNLTGPKDSDAARSLNK 623  
QY 441 -----AORLLKVDDIGLQNFN-----TTISLTSPSLALAVIR-----VNAS 479  
DB 624 LOKRERSCRAYQAMVETVNNL-LQOALNAWRDLTSDQLRAATMLDITVEESAFVLAD 682  
QY 480 SFNTTTFVAQDPANLQVSLQTPAPENSIGTITLPSL-----MNNLPAHDMELASR 530  
DB 683 NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPEPTGHGSTIQLSANTLKONGRNGEIR 742  
QY 531 VQNFPEET--PALFQDPSLENLSL-----ISYVSSSVANLTVRN-----LTR 571  
DB 743 VAFVLYNNLGPYL-----STENASMKLGTAMSTNHVSNVSPVITAAINKEFSNKVYLAD 798  
QY 572 NVTVTLKHNPSODELTVRVCFWDLGRNGRGSGDNGSVKDRRLNETICTCSHLTSFG 631  
DB 799 PVVFTVKHKKOSEENFNPCSFWSYKRTMTGYWSTQGCRLLTNNKTHTTCSNHLTNFA 858  
QY 632 VLL---DLSRTSVLPQAOMMALFTIYIGCGLSIFLSVTLVTVIAIEKIRRDYPSKILIQ 688  
DB 859 VLMAHVEVKHSDAV--HDLLEDVITWVGILLSVCLLCIETFCFFRGLQSD--RNTIHN 915  
QY 689 LCAALLLNLFLL-----DSWIALYKMOGLCISVAVFLHYFLVSVTWGMEAFHMYLA 743  
DB 916 LCISLFAELLELIGINRTDQPIA-----CAVFAALLHFFFLAAFTWMELEGVQLYIM 968  
QY 744 LVKVFNT--YIRKYILKFCIVGWGPVAVVTVITLISPDNYGLSGYKFPNGSPDDFCWI 801  
DB 969 LVEVESEHSRKY---FYLVGYGMPALIVAVSAADVRSYG-----TDKVCWL 1014  
QY 802 NNNAVFTYVVGFCVIFLLNVSMFIVLVOLCRICK--KKQLGAQRKTSIQDLR----- 854  
DB 1015 RLDTYFIWISFGPATLIIMLVIFGLIYALYKMFHHTAILKPEGCLDNTEDNRPFTKS 1074  
QY 855 ---SIAGLTFLLGITWGAFFAWGPNVNTFMVLFALFNTLQGGFFIFIFYCVAKENVRKOW 911  
DB 1075 WVGITALLCLLGLTWAFGLMYNESTVIMAYLFTIENSLOGMFIFIFCHVLOKKVRKEY 1134  
QY 912 RRYL---CCGKRLAENSOWSKTATNGLKKQTVNOGVSSSSNSLOSSNSTNTLLVNN 968  
DB 1135 GKCLRTHCCSG-RSTESSIGSGTSGSRTPGRYSTGQSRIRRMWMDTVRKQSESSFITG 1193  
QY 969 DCSVIASNGNASTERN-GVSFSV 991  
DB 1194 DINSSASLNREPRTSMGVKLN 1217

RESULT 12  
T18393  
latrophilin-3, splice variant abbg, brain-specific - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T18393  
R:Matsumita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.  
FEBS Lett. 443, 348-352, 1999  
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with diffd

## RESULT 13

tl8408  
latrophilin-3, splice variant bb9g, brain-specific - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T18408  
R:Matsushita, H.; Lelianova, V.G.; Ushkaryov, Y.A.  
FEBS Lett. 443, 348-352, 1999  
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with different alternative splicing  
A:Reference number: Z18869; MUID:99148828  
A:Accession: T18408  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Residues: 1-1308 <MAT>  
A:Molecule type: mRNA  
A:Cross-references: EMBL:AF111095; NID:94164072; PID:94164073; PIDN:AAD05331.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent  
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 10.0%; Score 533.5; DB 2; Length 1308;  
Best Local Similarity 24.2%; Pred. No. 6e-23;  
Matches 209; Conservative 123; Mismatches 345; Indels 187; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1273;  
Best Local Similarity 24.1%; Pred. No. 7.1e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T17188  
R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17188  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1273 <SUG>  
A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

QY 855 ---SIAGLTFLLGITWGFAPFANGPVVNTFMYLFAIFNTLQOFFIFIFCYCAKENVRKQW 911  
Db 1143 WVGATALLCLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFHCVLQKKRKEY 1202  
QY 912 RRYL---CCGKRLAENSQWKTATNGLKKQTVNOGVSSSSNSLOSSNSTSTTLLVNN 968  
Db 1203 GKCLRTHCCSG-RSTESSIGSGKTSGRTPGYSQSRIRRMWNTIVRKQSESSFITG 1261  
QY 969 DCSVHASGNGNASTERN-GVSFSV 991  
Db 1262 DINSSASLNREPRTSMGVKLN 1285

## RESULT 14

T17188

CL3AC protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000

C:Accession: T17188

R:Sugita, S.; Tschchenko, K.; Khvotchev, M.; Sudhof, T.C.

submitted to the EMBL Data Library, July 1998

A:Description: CL family.

A:Reference number: Z18712

A:Accession: T17188

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1273 &lt;SUG&gt;

A:Cross-references: EMBL:AF081156; NID:G3695139; PID:G3695139; PIDN:AAC62662.1

C:Superfamily: alpha-latrotoxin receptor, calcium-independent

## Query Match

Best Local Similarity 24.1%; Pred. No. 7.1e-23;

Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;

QY 248 SSPEELKQCLDQPIVCLADHPRGPPFSSQSIPVPRATVLSQVPRKATSFAPDPDYS 307

Db 398 SGPVHGVSV-ISPPIHLSDLERPPVRGISTGPGMGSTTTSTLRTTNLGRSTT 456

QY 308 PV-----THNVPSPIGEIQPLSPDPSAPIASPAIDMPQSETISSPMQTHVSGTTP 360

Db 457 PSLGRRNRSTSTSP--AIEVLDTHTLPSAASQIPAMEESCEAVEAREIMWFKTRQOQ 514

QY 361 PVKASFSSPTVS-----APANVTTSAPPVQTDIVNTSSISDLENQVLOMEKALSLS 413

Db 515 VAKOSCPAGTIGVSTYLCIAPDGIWDPQGP-----DLSNCS--SPWNHITOKLKS---GE 565

QY 414 LEPNLAGEMINOVSRLLHS-----PPDMLAPL-----PPDMLAPL----- 440

Db 566 TAANIARELAEQTRNHLNAGDITYSVRAMDQVLGLDVLQRLNLTTPGKDSARSINKLQK 625

QY 441 -----AORLLKVVDDIGLQNFN-----TTISLTSPSLALAVIR-----VNASEN 482

Db 626 RERSCRAYVOAMVETVNNL-LQPALNARDLTSDQLRAATMLLDTVEESAFVADNL 684

QY 483 TTTTVAQDPANLQVLETQAPENSIGTITLPSL-----MNNLPAHDMELASRVQF 533

Db 685 KTDIVRENTDNIQLEVARLSTEGNLEDKFPENTGHGTTIQLSANTLKQNGRGEIRVAF 744

QY 534 NFET--PALFQDPSPLENLSL-----ISYVTSVSSVANLTVRN-----LTRNVT 574

Db 745 VLXNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAANKFNSKVYLADPV 800

QY 575 VTLKHINPSODELTVRCVFWDLGRNGRGWSGSDNGSVKDRRLNETICTCSHLTSGVLL 634

Db 801 FTVKHIQSEENFNPCSFWSYKRTMTGWSTQGCRLTNTKTHTTCSNHLNFVLM 860

QY 635 ---DLSTSVLPAAOMALFTIYIGCGSSIFLSVTLVTYIAFEKIRRDYPSKILQICA 691

Db 861 AHVEVKHSDAV--HDLLDVTWVGILLSLVCLLCIFCFCFRGLQSD--RNTIKNLCI 917

QY 692 ALLLLNLVFL-----DSWIALYKMQGLCISVAVFLHYFLVSTWMLGFAFHYLALVK 746

Db 746

Db 918 SLFVAELLFLIGINRTDPIA-----CAVFAALLHFFELAAFTWMELEGVQLYIMLVE 970  
Qy 747 VFNT--YIRKYLKFCIVGVGVPVAVVTIITISPDNYGLSGYKGFPGSPDDFCWNNN 804  
Db 971 VFSEHSRRKY---FYLVGGMPLIIVAVSAADYRSYG-----TDKVCWLRD 1016  
Qy 805 AVFYIVVGVFCVIFLLNVSMFIVVLVQLCRIKK--KKOLGAQRKTSIQDLRSIAGLTFL 862  
Db 1017 TYFWSFIGPATLIIMLVNIFLGLYALYKMFHHTAILKPESGCLDNKISWVIGAI-A-LLCL 1075  
Qy 863 LGITWGAFFAWGPNVTFMYLFAFNTLQGFIFFYCVAKENVRKQW----RRYLCCG 918  
Db 1076 LGLTWAFGLMYNESTVIMAYLFTFNSLQGMFIFHCVLQKVKRKEYGKCLRTHCCSG 1135  
Qy 919 KL-----RLAENSND-----WSKTATNGLKQTVNQGVSNNSSLSQSS 955  
Db 1136 KSTESSIGSGKTSRTPGRYSTGOSRIRRWNDT---VRKQSESSFITGDINSASL 1191  
Qy 956 SNSTNSTLLVNNDCSVHASGN 977  
Db 1192 NRGTMANHLMSNALLRPHGTNN 1213  
RESULT 15  
T17200  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T17200  
R:Sugita, S.; Ichchenko, K.; Khvotchev, M.; Sudhof, T.C.  
submitted to the EMBL Data Library, July 1998  
A:Description: CL family.  
A:Reference number: Z18712  
A:Accession: T17200  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1341 <SUG>  
A:Cross-references: EMBL:AF081159; NID:g3695144; PID:g3695145; PIDN:AAC62665.1  
C:Superfamily: alpha-latrototoxin receptor, calcium-independent

Query Match 9.9%; Score 532; DB 2; Length 1341;  
Best Local Similarity 24.1%; Pred. No. 7.6e-23;  
Matches 208; Conservative 130; Mismatches 346; Indels 178; Gaps 31;  
Qy 248 SSPBELGLQCDLQDPFIVCLADHPRGPPSSSQSIPVVPRTATVLSQVPKATSAEPDPYS 307  
Db 466 GSPVHHGVSY-ISPPIHLDSDLERPPVVRGISTGTLGMSGTTTTLRTTWNLGRSTT 524  
Qy 308 PV-----THNVPSPGIEIQLSPQSPAPIASSPAIDMPPOSETISSPMPQTHVSGTTP 360  
Db 525 PSLPGRNRNSTSPSP--AIEVLDTVTHLPSAASQIPAMEESCEAVEAREIMWFKTRQGQ 582  
Qy 361 PVKASFSPTVS-----APANVNTTSAPPVGTDIVNTSSISDLENQVLQMEKALSIGS 413  
Db 593 VAKQSCPACTIGVSYLCLAPDGIWDPQ--DLSNCS-SPVWNHITQKLKS--GE 633  
Qy 414 LEPNLAGEMINOVSRLLHS-----PDMLAPL----- 440  
Db 634 TAANTARELAEOETHNLNAGDITYSVRAMDQLVGLLDVQLNLTTPGGKDSAAKSLNKLQK 693  
Qy 441 -----AORLLKVDDIGIQLNFSN-----TTISLTPSLALAVIR-----VNASSFN 482  
Db 694 RERSCRAYVQAMVETVNNL-LQPQALNWRDLTTSQDLRAATMLLDVRSFAVLADNLL 752  
Qy 483 TTFVQAQDPANLQVSLQETQAPENSIGTITLPSL-----MNNLPAMDMLASRVQF 533  
Db 753 KTDIVRENTDNIQLEVARLSTEGNLEDKLPENTGHGTSIOLSANTLKQNGRNGEIRVAF 812  
Qy 534 NFET--PALFOQPSLENLSL-----ISYVSSSVANLTVRN-----LTRNVT 574  
Db 813 VLYNNLGPYL-----STENASMKLGTTEAMSTNHSVIVNPSVITAANKFNSKNVYLDAPV 868

Qy 575 VTLKHINPSODELIVRCVFWDLGRNGRGSGSDNGSCVKDRRLNETICTCSHLTSEGVLL 634  
Db 869 FTVKHIKQSEENFNPCSWFSYSKRTMGYSTQCRLLTNTKHTTCSCNHLTNEAVLM 928  
Qy 635 ---DLSTRSVLPAQMMALTEITYIGCGLSISFSLVTLVYIAFEKIRRDYPPSKILQLCA 691  
Db 929 AHVEVKHSDAV--HDLDDVITWVIGILLSLVCLLCIFCFEFGLOSD-RNTIHRNLCL 985  
Qy 692 ALLLINLVFL-----DSWIALYKMOGLCSISAVFLHYFLVLSFTWGLAEAFHYIALVK 746  
Db 986 SLFVAELLFLIGINRTDPIA-----CAVFAALLHFFELAAFTWMELEGVQLYIMLVE 1038  
Qy 747 VFNT--YIRKYLKFCIVGVGVPVAVVTIITISPDNYGLSGYKGFPGSPDDFCWNNN 804  
Db 1039 VFSEHSRRKY---FYLVGGMPLIIVAVSAADYRSYG-----TDKVCWLRD 1084  
Qy 805 AVFYIVVGVFCVIFLLNVSMFIVVLVQLCRIKK--KKOLGAQRKTSIQDLRSIAGLTFL 862  
Db 1085 TYFWSFIGPATLIIMLVNIFLGLYALYKMFHHTAILKPESGCLDNKISWVIGAI-A-LLCL 1143  
Qy 863 LGITWGAFFAWGPNVTFMYLFAFNTLQGFIFFYCVAKENVRKQW----RRYLCCG 918  
Db 1144 LGLTWAFGLMYNESTVIMAYLFTFNSLQGMFIFHCVLQKVKRKEYGKCLRTHCCSG 1203  
Qy 919 KL-----RLAENSND-----WSKTATNGLKQTVNQGVSNNSSLSQSS 955  
Db 1204 KSTESSIGSGKTSRTPGRYSTGOSRIRRWNDT---VRKQSESSFITGDINSASL 1259  
Qy 956 SNSTNSTLLVNNDCSVHASGN 977  
Db 1260 NRGTMANHLMSNALLRPHGTNN 1281  
RESULT 16  
T18381  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T18381  
R:Matsushita, H.; Lellanova, V.G.; Ushkaryov, Y.A.  
FEBS Lett. 443, 348-352, 1999  
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di  
A:Reference number: Z18869; MUID:99148828  
A:Accession: T18381  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1407 <MAT>  
A:Cross-references: EMBL:AF111077; NID:94164036; PID:94164037; PIDN:AAD05313.1  
C:Superfamily: alpha-latrototoxin receptor, calcium-independent  
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 9.9%; Score 531.5; DB 2; Length 1407;  
Best Local Similarity 24.2%; Pred. No. 8.7e-23;  
Matches 258; Conservative 161; Mismatches 422; Indels 225; Gaps 48;  
Qy 90 VETTSND-----VTLSLPSN-----ETEKTITIVKTFNAGVKPKQ 128  
Db 188 IEVASLEDQNSRQITTYKLPNVRDGTGFVYDGAFFENKERTR-NIVYDLRTRIKSGE 246  
Qy 129 NTCNLSSICNDASAFFRG---EIMPOYDKES-----TVPQNHITNGTLTGVLSELKES 180  
Db 247 AINYANYHDTSPYRWGGKTDIDLAVDENGLWVIYATEQN-----NGMIVISOLNDY 298  
Qy 181 ELNKTQLTSETYFIMCATAEAOSTLACTFTIKL-----NNTMNAACAALAEKVRKIRME 236  
Db 299 TLR--FEATWETVYDKRAANAFMICGVLYVRSYQDNSESTCKNAIDYIYNTRNRCGE 356  
Qy 237 HCCCSVRIPCSPSEELGKQLQCDLPVCLADH-----PRGPP-----FS 277  
Db 357 Y-----VDVPEPNQYQYIAADVNDPRDNLQYVWNNNFILRYSLEFGPPDPAQVPTTAVTIT 412  
Qy 278 SSOSI---PVVPRTATVLSQVPKATSA-----EPPDYSPVTHNVPSPGIEIQLPS 324

Db 413 SSAEMFKTTVTSTTSQKPMSTTVAGSQEGSKGTAPPVAVS--TTKIP-PVTNIFPL- 468  
QY 325 PQPSAPIASSPAIDMP---POSE---TTSPPMPTQVHSGTPPPVKASFSPSTVSAPANV 377  
Db 469 -----PERFCALDARGIRWPOTQRMVVERPCPK---GT-----RGTASYLCVL 510  
QY 378 NTTAPPVQTDIVNTSS---ISDLENQVLOMEKALSIG-----SLEPNLAGEMINOVSR 429  
Db 511 STGTWNPKPDLNCTSHVWNLQAQIRSCENASLANELAKHTKGPVAGDVSSV-RL 569  
QY 430 LHSPPDML-APLAQRLKVVDDIGIQLN--FSNNTISLTSPSLALAVIRNAS--SFNTTT 485  
Db 570 MEQLVDIILDAQLELKPSEKDSAGRSYKALVDTVDNLLRPEALESWKHMNSSEQAHTAT 629  
QY 486 -----FVAQDPANL-----QVSLTEQ-----APENSIGITITLPSLMN----- 518  
Db 630 MLDDTLEGAFVLAD--NLVETRVSMPTENIVLEAVLSTEGQVQDFKFLGKAGSS 687  
QY 519 -NLPAHDMELASR---VQNFETFPALFQDPSLEN-----LSLSYVIVSS 559  
Db 688 IQLSANTVKQNSRNGKLAKLVFIYRSLGQFLSTENATIKLGADFIGRNSITAVNSHVISV 747  
QY 560 SVANLTVR-NLIRNVTVLKHNPSODELTVCVFDLGRNGRGGSNDGSCVKDRRLN 618  
Db 748 SINKESSRYLTDVPLFTPLHDP-DNYFNANCSEFNYSERTMGMYSTQCGKLVDTNKT 806  
QY 619 ETICTSHLTSGVLLDLSRTSVLP-AQMMALFTFIYIGCGLSSIFLSVLTVTYIAFEKI 677  
Db 807 RTTCACSHLTNFAILMAHREIAYKGVHLLLTIVTWGVIVSLVCAICIFTFFRGL 866  
QY 678 RRDYPSKILIOALALLNLVFLDLSWALYKMOGLCISVAVFLHYFLVFTWMLGEA 737  
Db 867 QSD-RNTIHKNLCLNLFIAETFLIG--IDTKYMIACPIFAGLLHFFELAAFAWMCLG 923  
QY 738 FMYLALVKVENT-YIRKYLKFCIVGMPVAVVVTIILTISPNDYGLSGYKFPNGSPD 796  
Db 924 VQLYMLVEFESEYSRKY--YYVAGYLFPATVGVSAADYKSYG-----TE 970  
QY 797 DFCWNNNAVYITVGVFCVIFLLNVSMFIVVLVOLCRICKKKQLGAQKRTSIQDLRS- 855  
Db 971 KACWLHVDNFIWFGPVTFIILLNI---IFLVITLCKMVKHNTLKPDSRLLENKSW 1027  
QY 856 IAG---LFTLLGITWGAFFAWPVPVNTFYLPFAINTTLOGFFIFPYCVAKENVRKOW- 911  
Db 1028 VLGAFAALLCLGLTWSFGLFNEETIIVMAYLFTIFNAPQGVFIHFICALQKVRREY 1087  
QY 912 ---RRYLCCGKL-----RLAENSQSKTATNGLKKTQVNOGVSSSSNSLQ 953  
Db 1088 KCFRHSYCCGGLPTESPSSHYKASTRTSARYSSTQSRIRRMWNTVRKQSSSFISGD 1147  
QY 954 SSNSTNSTLLVNNDCSVHAG-----NGNASTERNGVSFSVQNGD 995  
Db 1148 INSTSTLNOGHSNLNARDTSAMDTLPLNGFNFN-----SYSLRKGD 1188  
RESULT 17  
T14327  
alpha-latrotoxin receptor 3, calcium-independent - rat  
N:Alternate names: G-protein coupled receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: T14327  
R:Ichchenko, K.A.; Bittner, M.A.; Krasnoperov, V.; Little, A.R.; Chepurny, O.; Holz, R.  
J. Biol. Chem. 274, 5491-5498, 1999  
A:Title: A novel ubiquitously expressed alpha-latrotoxin receptor is a member of the CIR  
A:Reference number: Z17983; MUID:99150330  
A:Accession: T14327  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1550 <ICH>  
A:Cross-references: EMBL:AF063103; NID:G3882980; PID:G3882981; PIDN:AAC77816.1  
C:Genetics:

A:Gene: CIRL-3  
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.9%; Score 531.5; DB 2; Length 1550;  
Best Local Similarity 24.0%; Pred. No. 9.9e-23;  
Matches 216; Conservative 135; Mismatches 347; Indels 203; Gaps 35;

QY 248 SSPEELGKQLDQDPIVCLADHPRPSPSSOSIPVPRATVLSQVPKATSFABPPDYS 307  
Db 466 SGPVHHGVSY-ISPPIHLDSDLERPPVRGISTGTPLCMGSTTTTTLRTTTNLSRST 524  
QY 308 PV-----THNVPSPIGEIOPLSPQSPAPIASSPAIDMPQSEITSSPMPQTHVSGPPP 360  
Db 525 PSLGRRNRSTSPSP--AIEVLDTVTHLPSAASQIPAMEESCEAVEAREIMWFTRQOG 582  
QY 361 PVKASFSPSTVS-----APANVNTTSAPPVQTDIVNTSISDLENQVLOMEKALSLS 413  
Db 583 VAKQSCPAGTIGVSTYLCIADPGINDPQGP---DLSNCS--SPVNNHITOKLKS--GE 633  
QY 414 LEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440  
Db 634 TAANIARELAEQTRNLNAGDITYSVRAMDQLVGLDVLQRLNLTTPGKDSAAKSLQK 693  
QY 441 -----AQRLLKVVDIDIGLQNFEN-----TTISLTSPSLALAVIR---VNASSFN 482  
Db 694 RERSCRAYQVQAMVEIVNNL-LQPALNARDLTTSQLRATMLDITVEESAFVLADNLL 752  
QY 483 TTTTVAQDPANLQVLSLETOAPENSIGTITLPSL-----MNNLPAHDMELASRVQF 533  
Db 753 KTDIVRENTDNIQLEVARLSTEGNLEDLKFPEPNTGHGSTIQLSANTLKGNGRNGEIRVAF 812  
QY 534 NFEET--PALFQDPSLENLSL-----ISYVSSSYVANLTVRN-----LTRNVT 574  
Db 813 VLYNNLGPYL--STENASMKLGTEAMTNSHVSIVNPSVITAINKEFSKNVVLADPV 868  
QY 575 VTLKHINPSODELTVCVFDLGRNGRGGSVDNGSCVKDRRLNETICTCSHLTSFGVLL 634  
Db 869 FTVKHIKQSEENFNPCSFWSYSKRTMTGYWSTQGCRLLTNTKTHTTCSCHLNFEAVLM 928  
QY 635 ---DLSRTSLVPAQMMALFTFIYIGCGLSSIFLSVTLVYIAEKIRRDYPSKILIQICA 691  
Db 929 AHVEVKHSDAV--HDLLDVTITWVGILLSLVCLLICIFTFCFFRGLQSD-RNTIHKNLCI 985  
QY 692 ALLLLNLVFL--DSWIALYKMOGLCISVAVFLHYFLVFTWMLGEAFHMYLALVK 746  
Db 986 SLFVALLFLGINRTDQPIA-----CAVFAALLHFFFLAFTWMLFEGVQLIIMLVE 1038  
QY 747 VFNT--YIRKYLKFCIVGMPVAVVVTIILTISPNDYGLSGYKFPNGSPDPCWINNN 804  
Db 1039 VFBEHSRRKY---FYLVGYPALIVAVSAADVRSYG-----TDKVCWLRD 1084  
QY 805 AVFITYVGVFCVIFLLNVSMFIVVLVOLCRICK--KKQLGAQKRTSIQDLR----- 854  
Db 1085 TYFIWSFIGPATLILMLNIFLGIALYKMFHHTAILKPSGCLDNINVEDNRPFIKSWI 1144  
QY 855 SIAGLTFLLGITWGAFFAWPVPVNTFYLFALFNTLOGFFIFIFCYVAKENVRKOW--- 911  
Db 1145 GATALLCLGLTWAFGLMYINESTVIMAYLFTIFNSLQMGFIHFVCLVOKKVRKEGKC 1204  
QY 912 -RRYLCCGKL-----RLAENS-----WSKTATNGLKKTQVNOGVSS 947  
Db 1205 LRTHCCSKSTESSIGSGKTSGRTPRGYSTGSRIRRMWNT-----VRKQSESSFITG 1260  
QY 948 SSNSLOSSNSTNTTL-----LVNN--DCSVHAS--GNGNASTERNGVSFSVQNG 994  
Db 1261 DINSSASLNGSYLPCIQACVTYLEGLLNARDTSVMDTLPLNGN-----HGNSYSTAGG 1315  
QY 995 D 995  
Db 1316 E 1316

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QY 744 LKVKENT--YIRKYLKFCIVGWPVAVVVTIILTISPDNYGLSGYKFPNGSPDDFCWI 801  
 Db 1037 LVEVESESRKY---FYLVGMPALIVAVSAVRSYG-----TKVCWL 1082

QY 802 NNAVYITVVGFCVIFLNVSMFIVLVOLCRICK--KKOLGAQRKTSIQDLRSIAGL 859  
 Db 1083 RLDTYFIWFSFIGPATLIIMLVFLGIALYKMFHTAIKPKESGCLDNKISWVIGATA-L 1141

QY 860 TFLGITWGAFAFGVGVNVVTFMYLFAINTLQGFIFIFCYVAKENYKQWRVYL--C 916  
 Db 1142 LCLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFPHCVIQQKVKYKGLRTHC 1201

QY 917 CGKRLAENSDWSKTATNGLKKTQVNGVSSSSSSSLOSSTNSTTLLVNNDCSVHAG 976  
 Db 1202 CSG-RSTESSIGSGTSGKTPGYSTGSRIRRMWNTVYRKQSESEFICDINSASL 1260

QY 977 NGNASTERN-GVSFSV 991  
 Db 1261 NREPYRETSMGVKLNI 1276

RESULT 20  
 T18384  
 latrophilin-2 (splice variant bbabf) - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T18384  
 R: Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.  
 FEBS Lett. 443, 348-352, 1999  
 A: Title: The latrophilin family: multiply spliced G protein-coupled receptors with different  
 A: Reference number: Z18869; MUID: 99148828  
 A: Accession: T18384  
 A: Status: preliminary; translated from GB/EMBL/DBJ  
 A: Molecule type: mRNA  
 A: Residues: 1-1463 <MAT>  
 A: Cross-references: EMBL:AF111080; NID: g4164043; PID: g4164043; PIDN: AAD05316.1  
 C: Superfamily: alpha-latrototoxin receptor, calcium-independent  
 C: Keywords: alternative splicing; G protein-coupled receptor

Query Match 9.9%; Score 528.5; DB 2; Length 1465;  
 Best Local Similarity 22.9%; Pred. No. 1.4e-22;  
 Matches 259; Conservative 165; Mismatches 462; Indels 243; Gaps 46;

QY 90 VETSLND-----VTLSLPSN-----ETEKTITIVKTFNAGVKPQR 128  
 Db 188 IEYASLEDFQNSRQTTTKLPNRVDGTGFVYDGAVFENKERTR-NIVKYDLRTFIKSGE 246

QY 129 NICNLSSICNDSAFFRG---EIMFYDKES-----TVPQNHITNGTLTGVLSELKRS 180  
 Db 247 ALINYANYHDTSPYRWGKTDIDLAVDENGWLYIYATEQN-----NGMIVISQLNPY 298

QY 181 ELNKTLOTLSSETYFIMCATAEASTLNCFTFKL-----NNTMNACAAALALERVKIRPWE 236  
 Db 299 TLR--FEATWETVYDKRAASNAFMICGVLYVRSVQVDNESETEGKNAIDYINTRLNKE 356

QY 237 HCCSVRIPCSPSSPEELKQLQDLODPIVCLADH-----PRGPP-----FS 277  
 Db 357 Y-----VDVPFENQYIAADVNDPRNDQLYVNNNFILRYSLEEGPDPQAVPTAVTIT 412

QY 278 SSOSI---PVVPRATVLSQVPKATSA-----EPDPYSPVTHNVPSPIGEIQPLS 324  
 Db 413 SSAEMFTTSTTSQKGMSTTVAGSQEGSKGTPKAPPAVS--TTKIP--PVTNIFPL- 468

QY 325 PQSAPIASSPAIDMP-----POSE---TISSPMQTHVSGTTPPVKASFSPPTVAPANV 377  
 Db 469 -----PREFCALDARGTRWQTPQGMVVERCPK-----GT-----RGTSYLCVL 510

QY 378 NTSAPPVQTDIVNTSS--ISDLENQVLQMEKALSIG-----SLEPNLAGEMINQVSR 429  
 Db 511 STGWNFKGPDLSNCTSHWNQLAQKIRSGENASLANELAKTKGPVFGDVSSSV-RL 569

QY 430 LHSPPDML-APLAQRLLKVVDDIGLQLN--PSNTTISLTSPSLALAVIRVNAS-SENTTIT 485  
 Db 570 MEQLVDILDAQQLKPKSEKDSAGRSYNKAIVTDVNDLLRPEALESWKHMNSEQAHTAT 629

QY 486 -----FVAQDPANL-----QVSLETO-----APENSIGTITLPSLSMN----- 518  
 Db 630 MLDDTLEEGAFVLAD--NLVEPTFVSMPTENIVLEAVLSTEGVQDFKFLGKAGSS 687

QY 519 -NLPAHDMELASR---VQNFETPALFQDPSLEN-----LSLSIVSS 559  
 Db 688 IOLSANTVQKNSRGLAKLFIYIYRSIQGLSTENATIKLGADFTGRNSTIAVNSHVISV 747

QY 560 SVANLTVR-NLRTNVTVTLKHINPSODELTVRCVFDLGRNGRGWSDNGSCVSKDRRLN 618  
 Db 748 SINKESSRYLDDPVLTPLPHIDP-DNYFNANCSFWNYSERTMMGYWSQGCCKLVDTNKT 806

QY 619 ETICTCSHLTSEGVLLDLSRTSVLP-AQMMALTPITTYIGCLSSIFLSVTLVITYIAFEKI 677  
 Db 807 RTTCACSHLTNFAILLMAHREIAYKDGVHELLTVITVWGVIVISLCLATCICITFCFGRGL 866

QY 678 RRDYPSKILIQLCALLLNLLVFLDLSWIALYKMOGLCISVAVFLHYFLVLLVFTWGLEA 737  
 Db 867 QSD-RNTTHKNCLINLFIAEFIEFLG--IDTKYMIACPIFAGLLHFFFLAAFAWMCLEG 923

QY 738 FMYLALYKVFNT-YLRKYILKFCIVGWPVAVVVTIILTISPDNYGLSGYKFPNGSPD 796  
 Db 924 VOLYLMLVEVFESESRKYY--YVAGYLFPAVTVGVSAADYKSYG-----TE 970

QY 797 DFCWLNNAVYITVVGFCVIFLNVSMFIVLVOLCRICKKKKQKLGAKRTSIQDLRSI 856  
 Db 971 KACWLHVDNYFIWFSFIGPATLIIMLVFLGIALYKMFHTAIKPKESGCLDNKISWVIGATA 1030

QY 857 AG-----LTFELGITWGAFAFGVGVNVVTFMYLFAINTLQGFIFIFY 900  
 Db 1031 DGYNTDLPGSWLVGAFALLCLGLTWSFGLLFTNEETIVMAYLFTIFNAFGVFIPIFH 1090

QY 901 CVAKENVRKQW---RRYLCCGKRLAENSDWSKTAT-----NGL 936  
 Db 1091 CALOKKVRKEYGKCFRHSYCCGGLPTESPSSSVKASITRTSARYSSGQSRIRRMWNDIV 1150

QY 937 KKOIVNQGVSSSSSLOSSTNSTTLLVNNDCSVHAGNGNASTERNRGVSFVSQNGDV 996  
 Db 1151 RKQSESSFIGSDINSTSTLNQGMTGNLYLTNPLLRPHGTNNPNTYLLAETVVCNAPSAPV 1210

QY 997 CLHDFTKQHMFKNEKEDSC-----NGKGRMALRRTSKRGSILHETE 1036  
 Db 1211 ----FNSPGHSLNNARDTSAMDTPPLNGFNNSYSLRKGNDYNSVQVVD 1255

RESULT 21  
 T18386  
 latrophilin-2 (splice variant bbabf) - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T18386  
 R: Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.  
 FEBS Lett. 443, 348-352, 1999  
 A: Title: The latrophilin family: multiply spliced G protein-coupled receptors with di  
 A: Reference number: Z18869; MUID: 99148828  
 A: Accession: T18386  
 A: Status: preliminary; translated from GB/EMBL/DBJ  
 A: Molecule type: mRNA  
 A: Residues: 1-1463 <MAT>  
 A: Cross-references: EMBL:AF111082; NID: g4164046; PID: g4164047; PIDN: AAD05318.1  
 C: Superfamily: alpha-latrototoxin receptor, calcium-independent  
 C: Keywords: alternative splicing; G protein-coupled receptor

Query Match 9.9%; Score 527.5; DB 2; Length 1463;  
 Best Local Similarity 23.0%; Pred. No. 1.6e-22;  
 Matches 260; Conservative 168; Mismatches 455; Indels 247; Gaps 48;

QY 90 VETSLND-----VTLSLPSN-----ETEKTITIVKTFNAGVKPQR 128

Db	1208	V-----FNSPGHSLNNARDTSAMDTLPLNGNFNNNSYSLRKGNDYNDVQVVD	1253
RESULT	22		
T18383			
latrophilin-2, splice variant bbabe - bovine			
C:Species: Bos primigenius taurus (cattle)			
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000			
C:Accession: T18383			
R:Matsushita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.			
FEBS Lett. 443, 348-352, 1999			
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di			
A:Reference number: Z18869; MUID:99148828			
A:Accession: T18383			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-1422 <M>			
A:Cross-references: EMBL:AF111079; NID:g4164040; PID:g4164041; PIDN:AAD05315.1			
C:Superfamily: alpha-latrotoxin receptor, calcium-independent			
C:Keywords: alternative splicing; G protein-coupled receptor			
Query Match	9.8%	Score 526;	DB 2; Length 1422;
Best-Local Similarity	23.8%	Pred. No. 1.8e-22;	
Matches	257;	Conservative 158;	Mismatches 429; Indels 234; Gaps 46;
QY	90	VETTSLND-----VTLSLLPSN-----ETKTKITIVKTFNAGVVKPQR	128
Db	188	IEYASLEDFQNSRQTTTYTKLPNRVDGTGFVYDGVAFVFNKERTR-NIVKYDLRTRIKSGE	246
QY	129	NICNLSSICNDSAFFRG---EIMFYDKES-----TVPONQHTNGTLTGVLSELKRS	180
Db	247	AIINYANYHDTSPYRWGKTDIDLAVDENGWLWVIYATEQN-----NGMIVISQNLNY	298
QY	181	ELNKTQLTSETYFIMCATAEQAQSTLNCFTTKL-----NTMNAACAAIAALERVKIRPME	236
Db	299	TLR--FEATWETVYDKRAASNAFMICGVLYVRSVQDNSETEGKNAIDYIYNRLNRGE	356
QY	237	HCCSVRIPCSSPEELGKLDQDPIVCLADH-----PRGPP-----FS	277
Db	357	Y---VDVPFNOYQYIAADVNDPRDNLQYVNNNFILYSLEFGPPDPAQVPTTAVTIT	412
QY	278	SSQSI---PVVPRATVLSQVPRKATSA-----EPDYSPTVTHNVPSPICEIOPLS	324
Db	413	SSAEMFKTTVSTTTSOKGPMSTTVAGSQEGSKGKAPPAVS--TTKIP-PVTNIFPL-	468
QY	325	POPSAPIASSPAIDMP---POSE---TISSPMQTHVSGTTPPVKASFSSPTVSAPANV	377
Db	469	-----PERFCEALDARGIRWPQTRGMVVERPCPK---GT-----RGTASYLCVL	510
QY	378	NTTSAPPVQTDIVNTSS---ISDLENQVLOMEKALSIG-----SLEPNLAGEMINQVSR	429
Db	511	STGTWNPKGPDLSNCTSHWNQLAQKIRSGENAAASLANELAKHTKGFVAGDVSSV-RL	569
QY	430	LHSPDML-APLAQRLLKVVDIGLQLN--FSNTTSLTSPSLALAVIRYNAS--SEWTTT	485
Db	570	MEQLVDILDAQLELKPSEKDSAGRSYNAIVTDVNNLRPEALESWKHNSSQAHTAT	629
QY	486	-----FVAQDPANL---QVSLETQ-----APENSIGTITLPSLLMN-----	518
Db	630	MLLDLLEGAFLAD--NLVEPTRVSMPTENIVLEAVLSTEGOVQDFKPLGIKAGSS	687
QY	519	NLPAHDMELASR---VQNFNFTPALFQDPSLEN-----LSLISYVSS	559
Db	688	IQLSANTVKQNSRGLAKLVFIYRSLGQFLSTENATIKLGADFIGRSTAVNSHVISV	747
QY	560	SVANLTVR-NLNRNVTVTLKHINPSODELTVRCVFDLGRNGRGWGSDNGSCVKDRRLN	618
Db	748	SINKESSRVLLDPVLTPLPHIDP-DNYFNANCWFNYSERTWMGYWSTQCCKLVINDKT	806
QY	619	ETICFCSHLTSGVLLDLSRTSVLP-AQMMALFTIYIGGLSSIFLSVLTVYIAEPI	677
Db	807	RTTCACSHLTNFMAILMAHREIAYKDGVHELLLTAVITWVGIVISLVCLAICITFCFFRGL	866
Db	188	IEYASLEDFQNSRQTTTYTKLPNRVDGTGFVYDGVAFVFNKERTR-NIVKYDLRTRIKSGE	246
QY	129	NICNLSSICNDSAFFRG---EIMFYDKES-----TVPONQHTNGTLTGVLSELKRS	180
Db	247	AIINYANYHDTSPYRWGKTDIDLAVDENGWLWVIYATEQN-----NGMIVISQNLNY	298
QY	181	ELNKTQLTSETYFIMCATAEQAQSTLNCFTTKL-----NTMNAACAAIAALERVKIRPME	236
Db	299	TLR--FEATWETVYDKRAASNAFMICGVLYVRSVQDNSETEGKNAIDYIYNRLNRGE	356
QY	237	HCCSVRIPCSSPEELGKLDQDPIVCLADH-----PRGPP-----FS	277
Db	357	Y---VDVPFNOYQYIAADVNDPRDNLQYVNNNFILYSLEFGPPDPAQVPTTAVTIT	412
QY	278	SSQSI---PVVPRATVLSQVPRKATSA-----EPDYSPTVTHNVPSPICEIOPLS	324
Db	413	SSAEMFKTTVSTTTSOKGPMSTTVAGSQEGSKGKAPPAVS--TTKIP-PVTNIFPL-	468
QY	325	POPSAPIASSPAIDMP---POSE---TISSPMQTHVSGTTPPVKASFSSPTVSAPANV	377
Db	469	-----PERFCEALDARGIRWPQTRGMVVERPCPK---GT-----RGTASYLCVL	510
QY	378	NTTSAPPVQTDIVNTSS---ISDLENQVLOMEKALSIG-----SLEPNLAGEMINQVSR	429
Db	511	STGTWNPKGPDLSNCTSHWNQLAQKIRSGENAAASLANELAKHTKGFVAGDVSSV-RL	569
QY	430	LHSPDML-APLAQRLLKVVDIGLQLN--FSNTTSLTSPSLALAV	473
Db	570	MEQLVDILDAQLELKPSEKDSAGRSYNAIVTDVNNLRPEALESW	629
QY	474	IRYNAS--SEWTTT-----FVAQDPANL---QVSLETQ-----APENSIGT	509
Db	630	KHNSSQAHTATMLLTLEGAFLAD--NLVEPTRVSMPTENIVLEAVLSTEGOVQD	687
QY	510	ITLPSLLMN-----NLPAHDMELASR---VQNFNFTPALFQDPSLEN-----	549
Db	688	EKPLGIKAGSSIQLSANTVKQNSRGLAKLVFIYRSLGQFLSTENATIKLGADFIGR	747
QY	550	---LSLISYVSSVANLTVR-NLNRNVTVTLKHINPSODELTVRCVFDLGRNGRGWG	605
Db	748	NSTAVNSHVISINKESSRYITDPLFTPLPHIDP-DNYFNANCWFNYSERTWMGYW	806
QY	606	SDNGSVKDRRLNFTICTCSHLTSGVLLDLSRTSVLP-AQMMALFTIYIGGLSSIFL	664
Db	807	STQCKLVINDKTRTTACACSHLTNFMAILMAHREIAYKDGVHELLLTAVITWVGIVISLVCL	866
QY	665	SVTLVTYIAEPIKIRRDYPSKILIQCALALLNVLFLDLSWIALYKMOGLCISVAVFLHY	724
Db	867	AICITFCFFRGLQSD-RNTIHKNLINLFAEFTFLIG--IDTKYMIACPIFAGLLHP	923
QY	725	FLVSVFTWMLGEAFHMLYALVKVNT-VIRKYLKFCIVGCVGPAVVVTTILTISPDNYG	783
Db	924	FFLAAPAMCLEGVOLYMLMVEVESESRKY--YYVAGYLFPAIVGVSAIDYKSYG	981
QY	784	LGSYGKFPNGSPDDFCWINNAVFYITVVGFCYFIFLLNVMFIVVLVOLCRKIKKKQLG	843
Db	982	-----TERACWLHVDNYFIWFSIGPVTFTILLNI---IFLVITLCKMKVKSNTL	1027
QY	844	AQRKTSLODLRS-TAG---LIFLLGITWGAFFANGPVNVTWYLFPAINTLOGFFEIF	899
Db	1028	KPOSSRLNTKSWLGAFFALLCLLGLTWSFGLLFTNEETIVMAYLFTIENAFQGVFIIF	1087
QY	900	YVAKENVRKQW---RRYLCGKGLRLAENSOWSKTAT-----NG	935
Db	1088	HCAQKVKRYEYKCFRHSYCCGLPTESPSSVKASTTTSARYSSGTOSRIRRMNDT	1147
QY	936	LKQTVNQGVSSSNSLOSSNSTNTLLVNDGCVSHVAGSGNASTERNGVSFVQNGD	995
Db	1148	VRKQSESSFISGINDSTLTLNQGMTGNVLLTNPLLRPHGTNNPYNLTLLAETVVCNAPSAP	1207
QY	996	VCLHDFYTGKOHMFENEKEDSC-----NGKGRMALRRTSKRGLHETE	1036



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QY 441 -----AQRLLKVVDDIGLQLNFSN-----TTISTSPSLALAVIR-----VNASSFN 482
Db 694 RERSCRAYVQAMVETVNN--LQOALNAWROLTTSDQLRAATMLLDTVEESAFVLADNLL 752
QY 483 TTTFAQDPANLQVLESTQAPENSIGTTTLPSL-----MNNLPAHDMELASRVQF 533
Db 753 KDIVRENTNIOLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKGNGRNGEIRVAF 812
QY 534 NFRET--PALFQDPSLENLSL-----ISVYISSVANLTVRN-----LTRNVT 574
Db 813 VLXNNLGPYL-----STENASMKLGCTEAMSTNHSVTVNSPVITAANKFESKNVYLADPV 868
QY 575 VTLKHINPSQDELTVRCVFDLGRNGGCGSDGSCVKDRNLNETICTCSHLTSPGVLL 634
Db 869 FTVKHIKQSEENFNPNCSFWSYKRTMTGYSTOGCRLLTNNKTTCTSCNHLITNFVILM 928
QY 635 ---DLRSVLPQAOMMALTFITYIGCGLSSIFLSVTLVTYIAFERIRDPYSKILQLCA 691
Db 929 AHVEVKHSDAV--HDLLDLVITWVGILLSLVCLLCITFCFFERGLQSD--RNTIHKNLCL 985
QY 692 ALLLNLVFL-----DSWIALYKMGQICISVAVELHVLVFSFTWGLEAFHMYLALVK 746
Db 986 SLFAELLFLIGINRTDQPIA-----CAVEAALLHFFFLAAFTWMELEGVOLYIMLVE 1038
QY 747 VENT--YIRKYLKFCIVGWGPVAVVVTIILTISPDNYGLSGYKFPNGSPDDFCWINNN 804
Db 1039 VFSEHSRRKT---FYLGYGMPALIVAVSAADYRSYG-----TDKVCWLRD 1084
QY 805 AVEYITVVGFCVIFLLNVSMFIVVLVOLCRICK--KKQLGAQRKTSIQDLRSIAGLTLF 862
Db 1085 TYFTWFIGPATLIMLVNIFLGIALYKMFHRTAILKPESGCLDNKISWVIGAIA--LLCL 1143
QY 863 LGITWGAFFAWGPVNVTFMYLFAFNLTLOGFFIEFYCVAKENVRKQW---RRYLCCG 918
Db 1144 LGLTWAFGLMYINVESTVJMALFTIFNSLQGMFIIFHCVLQKKVKREYKGLURTHCCSG 1203
QY 919 FLRLAENSWSKTATNGLKQTVNGGVSSSSNSLOSSNST---NSTLLVNNDCSVHAS 975
Db 1204 K--STESSIGSGTSG--SRTPGRYSGSQSRIRRMWMDTVRKQSESSFITGDINSSAS 1258
QY 976 GNGNASTERN--GVSEFV 991
Db 1259 LNREPYRETSMGVXLNI 1275

RESULT 25
TI8385
latrophilin-2 (splice variant bbae) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: TI8385
R:Matsumita, H.; Lelianaova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with diff
A:Reference number: Z18869; MUID:99148828
A:Accession: TI8385
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1420 <MAT>
A:Cross-references: EMBL:AF111081; NID:g4164044; PID:g4164045; PIDN:AAD05317.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 9.8%; Score 525; DB 22; Length 1420;
Best Local Similarity 23.9%; Pred. No. 2.1e-22;
Matches 258; Conservative 161; Mismatches 422; Indels 238; Gaps 48;

QY 90 VETTSLND-----VTLSSLPSN-----EPEKTKITIVKTFNAGSVKRPQR 128
Db 188 IEYASLEDFQNSRQTQTYKPLNRVDGTGFVYDGAFFENKERTR-NIVKYDLRTRIKSGE 246
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Search completed: May 23, 2002, 07:39:39  
Job time: 198 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 23, 2002, 07:37:01 ; Search time 15.11 Seconds  
(without alignments)  
2659.887 Million cell updates/sec

CD97\_HUMAN CD97\_HUMAN STANDARD; PRT; 835 AA.  
 ID AC  
 P48960  
 01-FEB-1996 (Rel. 33, Created)  
 30-MAY-2000 (Rel. 39, Last sequence update)  
 01-MAR-2002 (Rel. 41, Last annotation update)  
 DT DT  
 DE Leucocyte antigen CD97 precursor.  
 GN CD97.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RX NCBI\_TaxID=9606;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=9536161; PubMed=7636245;  
 RA Hamann J., Eichler W., Hamann D., Kerstens H.M.J., Poddighe P.J.,  
 RT Hoovers J.M.N., Hartmann J.M.; Strauss M., van Lier R.A.W.;  
 RT "Expression cloning and chromosomal mapping of the leukocyte  
 RT activation antigen CD97, a new seven-span transmembrane molecule of  
 RT the secretory receptor superfamily with an unusual extracellular  
 RT domain.";  
 RT J. Immunol. 155:1942-1950(1995).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RP TISSUE=Foreskin;  
 RA MEDLINE=96230339; PubMed=8786105;  
 RT Hamann J., Hartmann E., van Lier R.A.W.;  
 RT "Structure of the human CD97 gene: exon shuffling has generated a new  
 RT type of seven-span transmembrane molecule related to the secretin  
 RT receptor superfamily.";  
 RT Genomics 32:144-147(1996).  
 RN [3]  
 REVISIONS.  
 RA Hamann J.;  
 RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: COULD BE A RECEPTOR POTENTIALLY INVOLVED IN BOTH  
 CC ADHESION AND SIGNALING PROCESSES EARLY AFTER LEUKOCYTE ACTIVATION.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS 1 GPS DOMAIN.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD97 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd97.htm".  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
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 CC EMBL; X84700; CAA59173.1; .  
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 DR EMBL; X94731; CAA64333.1; JOINED.  
 DR EMBL; X94732; CAA64333

RESULT 2  
EMRI\_MOUSE







Qy 936 ----LKKOTVNOGVSSSSNLSQSSSSNSTNTLLVND-----CSVHASGNGNASTERN 986  
 Db 1233 KDVLACQTV---LFKEVNTCNFTTGTLSRLSDEDEEPKSLVGPES-----1280  
 Qy 987 VSFVQNDV 996  
 Db 1281 LSFSLPGNI 1290  
 RESULT 5  
 BAI3\_HUMAN  
 ID BAI3\_HUMAN STANDARD; PRT: 1522 AA.  
 AC O60242; O60297;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Brain-specific angiogenesis inhibitor 3 precursor.  
 GN BAI3 OR KIAA0550.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RC TISSUE=Fetal brain;  
 RC MEDLINE=98194217; PubMed=9533023;  
 RX Shirtsuchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;  
 RA "Cloning and characterization of BAI2 and BAI3, novel genes homologous  
 RT to brain-specific angiogenesis inhibitor 1 (BAI1).";  
 RL Cytoget. Cell Genet. 79:103-108(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RC TISSUE=Brain;  
 RC MEDLINE=98290545; PubMed=9628581;  
 RX Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 5:31-39(1998).  
 CC -!- FUNCTION: MIGHT BE INVOLVED IN ANGIOGENESIS INHIBITION AND  
 CC SUPPRESSION OF GLOBLASTOMA.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN. ALSO DETECTED IN  
 CC HEART. REDUCED EXPRESSION IS OBSERVED IN SOME GLOBLASTOMA CELL  
 CC LINES.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 1 GPS DOMAIN.  
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 CC EMBL; AB005299; BAA25363.1; -  
 CC EMBL; AB011122; BAA25476.1; -  
 CC MIM; 602684; -  
 CC InterPro; IPR000859; CUB.  
 CC InterPro; IPR000832; GPCR\_secretin.  
 CC InterPro; IPR000203; PKD\_cys\_rich.  
 CC InterPro; IPR000884; TSP1.  
 CC InterPro; IPR001879; hormn\_receptor.  
 CC Pfam; PF00002; 7tm\_2; 1.  
 CC Pfam; PF01825; GPS; 1.  
 CC Pfam; PF02793; HRM; 1.

DR Pfam: PF00090; tsp\_1; 4.  
 DR SMART; SM00303; GFS; 1.  
 DR SMART; SM00008; Hormr; 1.  
 DR SMART; SM00209; TSP1; 4.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS0221; GPS; 1.  
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 DR PROSITE; PS00650; G-PROTEIN\_RECEP\_F2\_2; FALSE\_NEG.  
 DR PROSITE; PS0227; G-PROTEIN\_RECEP\_F2\_3; 1.  
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 DR PROSITE; PS0092; TSP1; 4.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Repeat; Alternative splicing.  
 FT SIGNAL 1 24  
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 Query Match 7.5%; Score 403; DB 1; Length 1522;  
 Best Local Similarity 23.5%; Pred. No. 5.7e-14;  
 Matches 160; Conservative 130; Mismatches 272; Indels 118; Gaps 31;

Qy 418 LAGEMINQVSRLLHSPDMLAPLQRLKLVDD----IGL-QLNFSNTTSLTSPSLALA 472  
 Db 648 IVSNLLDEENKEKWEQAQIYVPGSIELQVIEDTHIVGMMDFONS--YLMTGNVVAS 705  
 Qy 473 VIRVNASSFNITTFVAQDPANLQVLETOAPENSIGTITLPSLSMNNLPAHDMELASRVQ 532  
 Db 706 IQKLPAASVLTLD---INFPMKGRKGMVDWA-RNSEDRVVPKSIPTPVSKELDESS-- 758  
 Qy 533 FNFFETPALFOD-----PSLENLSLISVIVSSVANLTVRNLTNRN---VTVTLKHNPS 583  
 Db 759 -VFVLGAVLYKNLDLIPLTLRNYT-----VINSKIIVTIRPEKPTDTSFLELAHL--A 811

QY	584	QDELAVRCVFWDLGR--NGRGSGSDNGSCVVKDRRLNETICTCSHLTSGVLVLDLRSVTL	642	CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LIKELY TO BE
CC				CC	CONCENTRATED AT CELL-CELL ADHESION SITES.
CC				CC	-!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN. REDUCED OR NO
CC	812	NGTLNPNYCVLWDDSKTNESLGTWGTGCKTVLTDASHTKCLCDRLSTFAILAAQQAQPREILIM	871	CC	EXPRESSION IS OBSERVED IN SOME GLIOBLASTOMA CELL LINES AND CANCER
CC				CC	TISSUES.
CC				CC	-!- INDUCTION: BY P53.
CC	643	PAQ--MMALFFITVIGCLSSIFSVTLVTVIAFEKIRRDYPSKILIQCAALLNLNVLFL	701	CC	-!- DOMAIN: THE TSP1 REPEATS INHIBIT IN VIVO ANGIOGENESIS IN RAT
CC				CC	CORNEA INDUCED BY BFGF.
CC	872	ESSGTPSVTLI--VSGSLSCALITLAVVAALWRYIRSESIILNFCLSIISSNILL	929	CC	-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC				CC	-!- SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
CC	702	LDSWIALYKMOGLCISVAVFLHYFLVSVFTWMGLEAFHMYLALV-KVNTYIRKYILKFC	760	CC	-!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC				CC	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
CC	930	VGQTOHKN--SICTTTTAEHLFFELASFQWLVTEAWQSYMAVTKIRTLIRK--REFL	984	CC	BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION
CC				CC	AT THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC	761	IVGQWGPVAVV--TILITISPDNVLGSGYKFPNGSPDFCWINNNNAVYIITVGVFCVIF	819	CC	USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC				CC	MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC	985	CLGWLFPALVAVTSVGTFRKGYG-----TDHYCWLSEGLGLLYAFVGPAAAVV	1033	CC	ENTITIES REQUIRES A LICENSE AGREEMENT (SEE <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC				CC	OR SEND AN EMAIL TO <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC				CC	-----
CC	820	LLNVSMFIVVLVOLCR-----IKKKKOLGAQ-----RKTSIQDLRSIAGLTF-	861	CC	EMBL; AB005297; BAA23647.1; -
CC				CC	MIM; 602682; -
CC	1034	LVNVVIGILVFNKLVSRDGLDKLKHRAQOMSEPHSGILTKCAKCGVSVTTALSATTAS	1093	CC	InterPro; IPR000832; GPCR_secretin.
CC				CC	InterPro; IPR000203; PKD_cys_rich.
CC	862	-----LLGITWGFAPFAM--GPVNVTFMYLFAINTLQGFIFIFYCVAKEN	906	CC	InterPro; IPR000884; TSP1.
CC				CC	InterPro; IPR001879; hormo_receptor.
CC	1094	NAMASLWSSCWLPPLALTWMSAVLAWTDKRSILFQILFAVFDLSLOGFVIVMVHCILRRE	1153	CC	InterPro; PFO0002; 7tm_2; 1.
CC				CC	Pfam; PFO1825; GPS; 1.
CC	907	VRKOWRYLCCGKRLAE--NSDWSKTATNGLKK--QTVNQGVSSSNSL-----Q	953	CC	Pfam; PFO2793; HRM; 1.
CC				CC	Pfam; PFO0090; tsp_1; 5.
CC	1154	VQDAFR-----C-RLRNCQDPINADSSSPFNHQAQIMTDFEKDVIDIACRSVLHKDGPGR	1208	CC	SMART; SM00303; GPS; 1.
CC				CC	SMART; SM00008; HORMR; 1.
CC	954	SSSNSTNTSTLLVNDCSVHASGNNGASTENGVSFVSVONGD-----VCLHDTGTQKOHM--	1007	CC	SMART; SM00209; TSP1; 5.
CC				CC	PROSITE; PS0221; GPS; 1.
CC	1209	AATITGTLRSILND-----BEEKGTNPEGLSYSTLPNGNVISKVITIQPTG-LHNP	1260	CC	PROSITE; PS00649; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
CC				CC	PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
CC	1008	-FNEKEDSCNGKGRMARLRT	1026	CC	PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
CC				CC	PROSITE; PS0092; TSP1; 5.
CC	1261	SMNELSNPCLKKENSELRLT	1280	CC	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC				CC	Repeat; Cell adhesion.
CC				CC	POTENTIAL.
CC	RESULT 6			CC	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1.
CC	BAIL_HUMAN			CC	EXTRACELLULAR (POTENTIAL).
CC	AC	O14514; 2001 (Rel. 40, Created)		CC	1 (POTENTIAL).
CC	DT	16-OCT-2001 (Rel. 40, Last sequence update)		CC	CYTOPLASMIC (POTENTIAL).
CC	DT	01-MAR-2002 (Rel. 41, Last annotation update)		CC	2 (POTENTIAL).
CC	DE	Brain-specific angiogenesis inhibitor 1 precursor.		CC	EXTRACELLULAR (POTENTIAL).
CC	GN	BAIL		CC	3 (POTENTIAL).
CC	OS	Homo sapiens (Human)		CC	CYTOPLASMIC (POTENTIAL).
CC	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		CC	EXTRACELLULAR (POTENTIAL).
CC	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		CC	CYTOPLASMIC (POTENTIAL).
CC	OX	NCBI_TaxID=9606;		CC	EXTRACELLULAR (POTENTIAL).
CC	RN	[1]		CC	5 (POTENTIAL).
CC	RP	SEQUENCE FROM N.A.		CC	CYTOPLASMIC (POTENTIAL).
CC	RC	TISSUE=Fetal brain;		CC	6 (POTENTIAL).
CC	RA	MEDLINE=98054121; PubMed=9393972;		CC	EXTRACELLULAR (POTENTIAL).
CC	RA	Nishimori H., Shiratsuchi T., Urano T., Kimura Y., Kiyono K.,		CC	7 (POTENTIAL).
CC	RA	Tatsumi K., Yoshida S., Ono M., Kuwano M., Nakamura Y., Tokino T.;		CC	CYTOPLASMIC (POTENTIAL).
CC	RT	"A novel brain-specific p53-target gene, BAIL, containing		CC	TSP TYPE-1 1.
CC	RT	thrombospondin type 1 repeats inhibits experimental angiogenesis.";		CC	TSP TYPE-1 2.
CC	RL	Oncogene 15:2145-2150(1997).		CC	TSP TYPE-1 3.
CC	RN	[2]		CC	TSP TYPE-1 4.
CC	RP	INTERACTION WITH BAP1.		CC	TSP TYPE-1 5.
CC	RP	MEDLINE=98321173; PubMed=9647739;		CC	GPS.
CC	RA	Shiratsuchi T., Futamura M., Oda K., Nishimori H., Nakamura Y.,		CC	POLY-PRO.
CC	RA	Tokino T.;		CC	POLY-PRO.
CC	RT	"Cloning and characterization of BAI-associated protein 1: a PDZ		CC	CELL ATTACHMENT SITE (POTENTIAL).
CC	RT	domain-containing protein that interacts with BAIL.";		CC	NECESSARY FOR INTERACTION WITH BAP1.
CC	RL	Biochem. Biophys. Res. Commun. 247:597-604(1998).		CC	INDISPENSABLE FOR INTERACTION WITH BAP1.
CC	CC	-!- FUNCTION: LIKELY TO BE A POTENT INHIBITOR OF ANGIOGENESIS IN		CC	N-LINKED (GLCNAC. . .) (POTENTIAL).
CC	CC	BRAIN AND MAY PLAY A SIGNIFICANT ROLE AS A MEDIATOR OF THE P53		CC	N-LINKED (GLCNAC. . .) (POTENTIAL).
CC	CC	SIGNAL IN SUPPRESSION OF GLIOBLASTOMA. MAY FUNCTION IN CELL		CC	N-LINKED (GLCNAC. . .) (POTENTIAL).
CC	CC	ADHESION AND SIGNAL TRANSDUCTION IN THE BRAIN.		CC	N-LINKED (GLCNAC. . .) (POTENTIAL).
CC				CC	

FT CARBOHYD 844 844 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 877 877 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 881 881 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1584 AA; 173531 MW; DEARF28C77874513 CRC64;

Query Match 7.1%; Score 379.5; DB 1; Length 1584;  
 Best Local Similarity 25.9%; Pred. No. 1.1e-12;  
 Matches 135; Conservative 89; Mismatches 188; Indels 109; Gaps 20;

QY 436 MLAPLAORLLKVVDD-----IGLQNFSTNTSLTSPSALAVIRVNASSFTNTTF----- 486  
 Db 733 LAGNAKELRLEVEDVDVDTGFRMKRLDAYQVDT-NLVLSIHKLPAAGDITSEFPMKGW 791  
 QY 487 -----VAQDPANLOVSL-----ETOAPENS---IGTITLPSLMNNLPAHDMELASRV 531  
 Db 792 RATGDWAKVPEDRVTSKVSFSTGLTEADEASVFVGIV-----LYRNL----- 835  
 QY 532 QNFETPALFQDPSPLENLSLISVIVSSVANLV-----RNLTRNVTVTLKHINPSQDEL 587  
 Db 836 -----GSFLALQRNTTVLNSKVISVTVPKPPRSRLTPIEFIAHMYNGTTNQ 882  
 QY 588 TVRCVFWD-----LGRNGRGWSDNGSCVKDRRLNETICTSHLTSGVLLDLRS-TS 640  
 Db 883 T--CILWDETVPSSAPPGLPMSWRGCRTPVLDALTRCLCDRLSTFAILQAQLSADAN 940  
 QY 641 VLPQAMMALTFITYIGGLSSIFSLVTLVYIAFEKIRRDYPSKILIQCALLLNLVF 700  
 Db 941 MEKATLPSTVLI--VCGGVSLTLLMLVIVSVWRYRISERSVILINFLCSISSNALI 998  
 QY 701 LLDSTALYKMOGLCTISAVFLHYFLVFTWMGLEAFHMYLALV-KVENTYRKYLKF 759  
 Db 999 LIGQTQTRNKV--MCTLVAAFLHFFELSSFCWLTEAQSYMAVTGHLNRLLRK---RF 1053  
 QY 760 CLVGGCVPAVVVITILTISPDNYGLSGYKFPNGSPDFCWNNNAVFIYVVGFCVIF 819  
 Db 1054 LCLGWLPLVVAISV-----GFTKAGYSTMYNMLSLEGGLLYAFVGPAAAVV 1103  
 QY 820 LNVSMFIYVLVOLCR-----IKKKOLGAQRKTSIQDLRSIAGLTFLGILTWGPAFA 873  
 Db 1104 LVNMVIGILVFNKLVSKDGITDKKLERAGA-----SLWSSCVLPLALTWMSAVLA 1156  
 QY 874 WGPVNVV-----EMVLAIFNTLQGFIFIFCYVAKENVR 908  
 Db 1157 -----VTDRSALFQILFAVFDSEGLEFVIVMVHCLIREVQ 1192

Query Match 4.8%; Score 259; DB 1; Length 441;  
 Best Local Similarity 21.9%; Pred. No. 5.2e-07;  
 Matches 114; Conservative 84; Mismatches 184; Indels 138; Gaps 21;

QY 463 SLTSPSLALAVIRVNASSFTNTTFVAODPANIQ-----VSETOAPENSIGTITLPSL 516  
 Db 9 ALEAAEAAAAAQAADAPTIT---PSPRTLQORACEALMEGDAPD----- 53  
 QY 517 MNLLPAHDMELASRVQFN-----FFETP--ALFQDPSPLENLSLISVIVSSVANLVTRNLT 570  
 Db 54 ----AAPAPLRCALIAWDGVNCWNPETPAGALAVQPCFDELINGIRYDIRQNAIRMCVSN-- 107  
 QY 571 RNVTVTLKHINFSQDELTVRCVFDLGRNGRGWSDNGSCVKDRRLNETICTSHLTSE 630  
 Db 108 -----GTWRNYSDYVHVCRELVEAEDS----- 128  
 QY 631 GVLLDLRSVLPQAMMALTFITYIGGLSSIFSLVTLVYIAFEKIRRDYPSKILIQCAL 690  
 Db 129 -----EDAAAFVFEVGFCLSLVAIAVAIWIFLYFKDL-RLCNTHTNTLM 173  
 QY 691 AALLLLNLVFLDSDWIALY-KMOGLCTISAVFLHYFLVFTWMGLEAFHMYLALVKNFN 749  
 Db 174 ATYICNDATWILSAVVOEYVENGGLCSVLAVLMHYFVLTNFFMFEVGLYFLVAVTF- 232  
 QY 750 TYIRKYILKFCITGVGVPAVVVITILTI-----SPDNYGLGS-----YGFPPNGSPDF 798  
 Db 233 TGEKVKLQIYIIIGWIPGVIVVTWAIKHLGKTAPDAPNAGESHPMVLKIKCPWMAEDYF 292

RESULT 7  
 ID DIHR\_ACHDO STANDARD; PRT; 441 AA.  
 AC Q16983;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Diuretic hormone receptor precursor (DH-R).  
 OS Acheta domestica (House cricket).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta; Gryllota; Neoptera; Orthoptera; Orthoptera; Ensifera; Gryllidae; Gryllinae; Acheta.  
 OC NCBI\_TaxID=6997;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Malpighian tubules;  
 RX MEDLINE=96189577; PubMed=8673074;  
 RA Reagan J.D.;  
 RT "Molecular cloning and function expression of a diuretic hormone receptor from the house cricket, Acheta domestica";  
 RL Insect Biochem. Mol. Biol. 26:1-6(1996).  
 CC -!- FUNCTION: RECEPTOR FOR THE INSECT DIURETIC HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MALPIGHIAN TUBULES.

-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
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CC EMBL; U15959; AAC47000.1; -  
 CC GCRdb; GCR\_1380; -  
 DR InterPro: IPR000832; GPCR\_secretin.  
 DR InterPro: IPR001879; hormu\_receptor.  
 DR Pfam: PF00002; 7tm\_2; 1.  
 DR Pfam: PF02793; HRM; 1.  
 DR PRINTS; PRO0249; GPCRSECRETIN.  
 DR SMART; SM00008; Hormr; 1.  
 DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
 DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 DR PROSITE; PS00227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE; PS00261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 ?  
 FT CHAIN ? 441  
 FT DOMAIN ? 134  
 FT TRANSMEM 135 158  
 FT DOMAIN 159 166  
 FT TRANSMEM 167 187  
 FT DOMAIN 188 194  
 FT TRANSMEM 195 224  
 FT DOMAIN 225 238  
 FT TRANSMEM 239 260  
 FT DOMAIN 261 291  
 FT TRANSMEM 292 315  
 FT DOMAIN 316 338  
 FT TRANSMEM 339 357  
 FT DOMAIN 358 371  
 FT TRANSMEM 372 391  
 FT DOMAIN 392 441  
 FT CARBOHYD 99 99  
 FT CARBOHYD 107 107  
 FT CARBOHYD 112 112  
 SQ SEQUENCE 441 AA; 49538 MW; 501915AC2E776C5C CRC64;

QY 799 CWINNNAVYTVVYGVPCVIFLLNVSMFIVLVOLCRKIKKQKLGQAQRKTSIODLRSIAG 858  
Db 293 DWIHOAPVITVLAVN---LVFLFSMMVLIITKLOSAENTAQQ---YRKAT---RALLV 342  
QY 859 LTFELGLTGWFAFFAWGPNVNTFELF---AIFNTLQOFFIFIFCYVAKENVR----- 908  
Db 343 LFLPLGLT---YILMQGPMDCVAGHVFNRNAQALLSLOGFTVALFYCFLENTEVONTLHRH 400  
QY 909 -KQW-----RRYLCCGKRLAENSWS-KTATNGLK 937  
Db 401 MSRWRETRTVGGRRYTLSG-----HSKDWSPRSRSTESIR 435

RESULT 8  
PACR\_MOUSE STANDARD; PRT; 496 AA.  
ID PACR\_MOUSE  
AC P70205;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pituitary adenylate cyclase activating polypeptide type I receptor  
DE precursor (PACAP type I receptor) (PACAP-R-1).  
GN ADCYAP1R1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96256640; PubMed=8664310;  
RA Hashimoto H., Yamamoto K., Hagiwara N., Ogawa N., Nishino A.,  
RA Aino H., Nogi H., Imanishi K., Matsuda T., Baba A.;  
RT "CDNA cloning of a mouse pituitary adenylate cyclase-activating  
RT polypeptide receptor.";  
RL Biochim. Biophys. Acta 1281:129-133(1996).  
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE  
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,  
CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND  
CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM  
CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE  
CC GASTROINTESTINAL TRACT.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; D82935; BAAL1639.1; -  
CC GCRDb; GCR\_1152; -  
CC MGD; MGI:108449; Adcyap1r1.  
CC InterPro; IPR000832; GPCR\_secretin.  
CC InterPro; IPR001879; hormn\_receptor.  
CC Pfam; PF00002; 7tm\_2; 1.  
CC Pfam; PF02793; HRM; 1.  
CC PRINTS; PR00249; GPCRSECRETIN.  
CC SMART; SM00008; Hormr; 1.  
CC PROSITE; PS00649; G.PROTEIN\_RECEP\_F2\_1; 1.  
CC PROSITE; PS00650; G.PROTEIN\_RECEP\_F2\_2; 1.  
CC PROSITE; PS00227; G.PROTEIN\_RECEP\_F2\_3; 1.  
CC PROSITE; PS00261; G.PROTEIN\_RECEP\_F2\_4; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
CC Spermatogenesis.  
KW SIGNAL 1 20 POTENTIAL.  
KW CHAIN 21 496 PITUITARY ADENYLATE CYCLASE ACTIVATING  
FT FT POLYPEPTIDE TYPE I RECEPTOR.  
FT FT EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 21 155

TRANSMEM 156 178 1 (POTENTIAL).  
FT DOMAIN 179 186 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 187 205 2 (POTENTIAL).  
FT DOMAIN 206 227 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 228 253 3 (POTENTIAL).  
FT DOMAIN 254 268 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 269 291 4 (POTENTIAL).  
FT DOMAIN 292 309 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 310 332 5 (POTENTIAL).  
FT DOMAIN 333 378 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 379 399 6 (POTENTIAL).  
FT DOMAIN 400 413 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 414 433 7 (POTENTIAL).  
FT DOMAIN 434 496 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 496 AA; 56639 MW; 47B5D51D4209060A CRC64;

Query Match 4.4%; Score 235; DB 1; Length 496;  
Best Local Similarity 22.6%; Pred. No. 1.1e-05;  
Matches 95; Conservative 75; Mismatches 145; Indels 106; Gaps 20;

QY 596 LQRNGRGWSD-----NGCSVKDRRLNETICTCSHLTSGVLLDLSRTSVLPQMMAL 649  
Db 114 VGRNCTEDGSEPFPHYFDACGFDYE-----PESGDQDYIYLSV 153  
QY 650 TPTITVIGCLSSIFLSVTLVTYIAFEKIR--RDYPSKILIQCAALLILNLVFLDWSIA 707  
Db 154 KALYTVGYSTSLVTLTAMVILCRFRKLHCTRNF---IHMNLFVSFMLRAISVEIKDWI- 209  
QY 708 LYKMOGL-----CISVAVELHYFLVSTWMLGLEAFHMYLALVKVFTYIRKYILK 758  
Db 210 LYAEODSSCHCFVSTVECKAVMVFHYCVWSNYEFLTEGLYFTLLVETTFPE-RRYFYW 268  
QY 759 FCIVGWGVAVVVTI--ILTISPDNYGLSGVGRNGSPDDFCWINNN--AVFYI---TV 811  
Db 269 YTIIGWTCTVCTVWVAVLRLYFDDAG-----CWMNDSTALWVVIKGPV 313  
QY 812 VGYFCVIFLLNYSMTFVL-----VOLCRKIKKQKLGQAQRKTSIOD 852  
Db 314 VGSIMVNFVLFIGIILILVQKLOSPDMGNGESSIYFCVQKCYC--KPQRAQQHCKMSE 371  
QY 853 LRSI-----AGLIFLLGITWG--FAFFAWGPNVT--PMYLFAL-FNTLOGFEIFICYV- 902  
Db 372 LSTITLRLARSTLLPLFEGIHVTFAFSPENVSKRERLVFELGLSGFGFVAVLYCFL 431  
QY 903 ---AKENVKQWRRLCCGKRLAENSWS---KTATNGLKKTQVNGVSSSSNSLOSS 955  
Db 432 NGEVQAEIRKKRWSW-----KVNRYFTWDFKIRHPSLASSGVNGGTQLSILSKSSQLRMS 487  
QY 956 S 956  
Db 488 S 488

RESULT 9  
ID CRFL\_SHEEP STANDARD; PRT; 415 AA.  
AC O62772;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRFL)  
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).  
GN CRHRL.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]

SEQUENCE FROM N.A.  
 TISSUE=pituitary;  
 MEDLINE=99079328; PubMed=9863624;  
 MYERS D.A., Trinh J.V., Myers T.R.;  
 "Structure and function of the ovine type 1 corticotropin releasing  
 factor receptor (CRF1) and a carboxyl-terminal variant.";  
 Mol. Cell. Endocrinol. 144:21-35(1998).  
 -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.  
 SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS  
 MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.  
 -!- SURCELLULAR LOCATION: Integral membrane protein.  
 -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.  
 -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 -----  
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EMBL; AF054582; AAC08027.1; -  
 InterPro; IPR000832; GPCR\_secretin.  
 InterPro; IPR001879; hormn\_receptor.  
 Pfam; PF00002; 7tm\_2; 1.  
 Pfam; PF02793; HRM; 1.  
 PRINTS; PR00249; GPCRSECRETIN.  
 SMART; SM00008; Hormr; 1.  
 PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; FALSE\_NEG.  
 PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_5; 1.  
 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 phosphorylation.  
 SIGNAL 1 24 POTENTIAL  
 CHAIN 25 415 CORTICOTROPIN RELEASING FACTOR RECEPTOR  
 1.  
 DOMAIN 25 121 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 122 142 1 (POTENTIAL).  
 DOMAIN 143 151 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 152 171 2 (POTENTIAL).  
 DOMAIN 172 189 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 190 213 3 (POTENTIAL).  
 DOMAIN 214 227 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 228 249 4 (POTENTIAL).  
 DOMAIN 250 268 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 269 291 5 (POTENTIAL).  
 DOMAIN 292 314 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 315 334 6 (POTENTIAL).  
 DOMAIN 335 349 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 350 369 7 (POTENTIAL).  
 DOMAIN 370 415 CYTOPLASMIC (POTENTIAL).  
 CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 78 78 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SEQUENCE 415 AA; 47558 MW; FA5F652D12B4CDC4 CRC64;

Query Match 4.3%; Score 232; DB 1; Length 415;  
 Best Local Similarity 25.2%; Pred. No. 1.3e-05;  
 Matches 105; Conservative 61; Mismatches 151; Indels 100; Gaps 23;  
 540 ALFQDPSLESLISYVSSVANLTNRNLTNRVTLTKHI-----NPSQDLTVR-CVWF 594  
 23 ASLDQHCESLSLAS-----NVSLQCNASVDLNGTCWPQSPA-GGLVVRPCLVF 71  
 595 DLG-----RNGR-----GMSDNGCSVKDRNLTICPSHLTISFGVLDLSRTSLVP 643  
 72 FYGVRYNTNSGYRCLANGTWA-----ARVNHNS--ECQEILSSEG---EKS----- 113

QY 644 AQMMALTFITYICGGLSSIFSLSVTLVYIAFEKIR--RDYPSKILLIQLCAALLLNVL 701  
 Db 114 AIYHIAIINYLG---HCISLAALLVAFVLEFLRLSIRCVRNIIHWNLSAFLRNA--- 167  
 QY 702 LDSWIALYKMQ-----GLCISVAVFLHYFLVLSFTWMLGFAFMVYALVKVENT-Y 751  
 Db 168 --TWVQLTMSPEVHQSNGVCLVTAANYFHTNFWMEGEGCYLHTAVVLT\*STDR 225  
 QY 752 IKKYILKFCIVGVV--PAVVVITLITSPDNYGLGSGYKPGSPDDFCWINNNAVFYI 809  
 Db 226 LRKWM--FICIGVGFPIIIVAMAIGKLYDN-----EKCWEFGKPGCVYT 268  
 QY 810 TVV--GYFCVIFLLNVMFIVLVQLCRKKKQOLGAORQTSIQDLRSTAG---LTFLLG 864  
 Db 269 DYIYOGPMILVLLIN---FIFLNFVIRILMTKLRASSTETIQYRKAVKATLVLLPLG 324  
 QY 865 ITWGAFFAWGP---VNVTFMYLFAITNTLQGFIFIEYCV----AKENVRKQWRY 914  
 Db 325 ITYMLFFVNPGEDEVSRVVFYFNSFLESFGFFSVFYCFNLSEVRSVRSIRKRWHEW 381  
 RESULT 10  
 ID CRF2\_XENLA STANDARD; PRT; 413 AA.  
 AC 042603;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Corticotropin releasing factor receptor 2 precursor (CRF-R 2) (CRF2)  
 GN (Corticotropin-releasing hormone receptor 2) (CRH-R 2).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, and Heart;  
 RX MEDLINE=97465573; PubMed=9326293;  
 RA Dautzenberg F.M., Dietrich K., Palchaudhuri M.R., Spiess J.;  
 RT "Identification of two corticotropin-releasing factor receptors from  
 RT Xenopus laevis with high ligand selectivity: unusual pharmacology of  
 RT the type 1 receptor.";  
 RL J. Neurochem. 69:1640-1649(1997).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.  
 CC SHOWS HIGH-AFFINITY BINDING FOR UROTENSIN I. THE ACTIVITY OF THIS  
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL  
 CC CYCLASE (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 EMBL; Y14037; CAA74364.1; -  
 GCRDB; GCR\_2578; -  
 InterPro; IPR000832; GPCR\_secretin.  
 InterPro; IPR001879; hormn\_receptor.  
 Pfam; PF00002; 7tm\_2; 1.  
 Pfam; PF02793; HRM; 1.  
 PRINTS; PR00249; GPCRSECRETIN.  
 SMART; SM00008; Hormr; 1.  
 PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
 PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_5; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 ? POTENTIAL.  
 FT CHAIN ? 413  
 FT  
 FT  
 FT DOMAIN ? 120 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 121 141 1 (POTENTIAL).  
 FT DOMAIN 142 150 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 151 170 2 (POTENTIAL).  
 FT DOMAIN 171 187 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 188 211 3 (POTENTIAL).  
 FT DOMAIN 212 225 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 226 247 4 (POTENTIAL).  
 FT DOMAIN 248 266 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 267 289 5 (POTENTIAL).  
 FT DOMAIN 290 312 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 313 332 6 (POTENTIAL).  
 FT DOMAIN 333 347 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 348 367 7 (POTENTIAL).  
 FT DOMAIN 368 413 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 413 AA; 48458 MW; DAD422F0A96C4626 CRC64;

Query Match 4.3%; Score 231.5; DB 1; Length 413;  
 Best Local Similarity 23.3%; Pred. No. 1.4e-05;  
 Matches 83; Conservative 63; Mismatches 127; Indels 83; Gaps 16;

QY 588 TVRCVFDLGRNGSGSDNGSCVKDRDLNETICPSHLTSFGLDLSRTSVLPQMM 647  
 DB 78 .TTRNVYRCFENGWASW-----MNYSQCV-----PILDNRKRYALHYKIA 118  
 QY 648 ALTFITYGGLSSIFSLVTLVYTAFAKIR--RDYPSKILIOLCRAALLNLVFL-- 702  
 DB 119 LI--INYLGHGISIALVIAFLFLCLRSICRLNT---IHNWLTITFLIRNMWFLQM 173  
 QY 703 -----DSNIALYKMGGLGISVAVFLHYFLVFTWGLFAFMYLALVKVFT--YI 752  
 DB 174 IDNHNESNFW-----CRCTITVYFVVTFFWMEVSGYLHTAIVTYSIDL 224  
 QY 753 RYILKFCIVGVPV--VWVTIITISPDNYGLSGYKPGPNPDPCWNNNAVYIT 810  
 DB 225 RKWV--FLFIGWCIPSPITVTAICKLFYEN-----EQCWIGKEPGKYID 267  
 QY 811 VV--GYFCVIFLLNMFVWLVLQCRKIKKQKOLGAQRKTSIOLRSIAG--LTFLLGI 865  
 DB 268 YIYOGRVILVLLN----FVFLNIVIRILMTKURASTTETIQYKAVKATLVLLPLGI 323  
 QY 866 TWGFAFFAWGPVNVV--PMYLFALFNTLQGFIFIFYCVAKENV-----RKQWRY 914  
 DB 324 TYMLFVNPGEDDVSQIVFIYFNSFLSQFGFPVSFYCFNLNGEVRSAAKRWHRW 379

RESULT 11  
 CRF1\_RAT STANDARD; PRT: 415 AA.  
 AC P35353;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)  
 DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).  
 GN CRHR1 OR CRHR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;  
 RX MEDLINE=94062694; PubMed=8243338;

Perrin M.H., Donaldson C.J., Chen R., Lewis K.A., Vale W.W.;  
 "Cloning and functional expression of a rat brain corticotropin  
 releasing factor (CRF) receptor.";  
 Endocrinology 133:3058-3061(1993).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=9409969; PubMed=8274282;  
 RA Chang C.P., Pearce R.V. II, O'Connell S., Rosenfeld M.G.;  
 "Identification of a seven transmembrane helix receptor for  
 corticotropin-releasing factor and sauvagine in mammalian brain.";  
 J. Biol. Chem. 271:14519-14525(1996).  
 RT Neuron 11:1187-1195(1993).  
 RL [3]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Testis;  
 RX MEDLINE=96278921; PubMed=8662941;  
 RA Tsai-Morris C., Buczek E., Geng Y., Gamboa-Pinto A., Dufau M.L.;  
 "The genomic structure of the rat corticotropin releasing factor  
 receptor. A member of the class II G protein-coupled receptors.";  
 J. Biol. Chem. 271:14519-14525(1996).  
 RT  
 RL  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.  
 CC SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS  
 CC MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: ENTIRE NERVOUS SYSTEM.  
 CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; L24096; ; NOT\_ANNOTATED\_CDS.  
 CC EMBL; L25438; AAA16441.1; .  
 CC EMBL; U53498; AAC53519.1; .  
 CC EMBL; U53486; AAC53519.1; JOINED.  
 CC EMBL; U53487; AAC53519.1; JOINED.  
 CC EMBL; U53488; AAC53519.1; JOINED.  
 CC EMBL; U53489; AAC53519.1; JOINED.  
 CC EMBL; U53490; AAC53519.1; JOINED.  
 CC EMBL; U53491; AAC53519.1; JOINED.  
 CC EMBL; U53492; AAC53519.1; JOINED.  
 CC EMBL; U53493; AAC53519.1; JOINED.  
 CC EMBL; U53494; AAC53519.1; JOINED.  
 CC EMBL; U53495; AAC53519.1; JOINED.  
 CC EMBL; U53496; AAC53519.1; JOINED.  
 CC EMBL; U53497; AAC53519.1; JOINED.  
 CC GCRDb; GCR\_0819; .  
 CC GCRDb; GCR\_0947; .  
 CC GCRDb; GCR\_1414; .  
 CC GCRDb; GCR\_1415; .  
 CC GCRDb; GCR\_1469; .  
 CC InterPro; IPR000832; GPCR\_secretin.  
 CC InterPro; IPR001879; hormn\_receptor.  
 CC Pfam; PF00002; 7tm\_2; 1.  
 CC Pfam; PF02793; HRM; 1.  
 CC PRINTS; PR00249; GPCRSECRETIN.  
 CC SMART; SM00008; Hormr; 1.  
 CC PROSITE; PS00649; G-PROTEIN\_RECEP\_F2\_1; 1.  
 CC PROSITE; PS00650; G-PROTEIN\_RECEP\_F2\_2; 1.  
 CC PROSITE; PS00277; G-PROTEIN\_RECEP\_F3; 1.  
 CC PROSITE; PS00261; G-PROTEIN\_RECEP\_F2\_4; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Phosphorylation.  
 KW SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 415 CORTICOTROPIN RELEASING FACTOR RECEPTOR  
 FT  
 FT DOMAIN 25 121 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 122 142 1 (POTENTIAL).  
 FT

FT DOMAIN 143 151 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 152 171 2 (POTENTIAL).  
 FT DOMAIN 172 189 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 190 213 3 (POTENTIAL).  
 FT DOMAIN 214 227 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 228 249 4 (POTENTIAL).  
 FT DOMAIN 250 268 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 269 291 5 (POTENTIAL).  
 FT DOMAIN 292 314 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 315 334 6 (POTENTIAL).  
 FT DOMAIN 335 349 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 350 369 7 (POTENTIAL).  
 FT DOMAIN 370 415 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 415 AA; 47842 MW; 48D6704B31D4C013 CRC64;  
 Query Match 4.3%; Score 230; DB 1; Length 415;  
 Best Local Similarity 25.4%; Pred. No. 1.7e-05;  
 Matches 103; Conservative 67; Mismatches 153; Indels 82; Gaps 22;  
 QY 543 QDPSLENLSLISYVSSVANLTVRNLTNRVTTLKHNPSQDELTVR-C-----VFWD 595  
 DB 26 QDQRCENLSL-----TSNVSLQC-NASVDLIGTCWPRSPA-QGLVVRPCPAFFYGVRYN 78  
 QY 596 LGRNGR-----GWSNDGCSVKDRNLNETICTCSHLTSGVLLDLSRTSVLPQMMALT 650  
 DB 79 TTNGYRECLANGWA-----ARVNVSECO-----EILNEEKSKV---HYHVAV 120  
 QY 651 FTIVYGGCLSSIFLSTVLTVYIAFEKIR--RDYPSKILIQALCALLLNLV-FLLDSWIA 707  
 DB 121 YINVLGHCISLVALVAFVFLRLRSICRLNI---IHNWLSAFILRNATVFWVQLTVS 177  
 QY 708 LYKMQ---GLCISAVAFVFLVFLVFTWGLFAFMYLALVKVFT-YIRKYLKFCIVG 763  
 DB 178 PEVHQSNVACRLVTAAYVYHVTNFFNFMFGEGCVLHTAIVLYSTDRLRKWM--FVCIG 235  
 QY 764 WGV--PAVVVTIILTISPNDYGLGSGYKFPNGSPDPCWINNNAVFYITVV--GYFCVIF 819  
 DB 236 WGVPEPIIWAIGLHVDN-----EKWFGKRPVYTDYIYOGPMILVL 280  
 QY 820 LLNVSMFIVLVQLCRKKKQKOLGAQRKTSIQDLRSIAG---LTFLLGITWGFAPFAWGP 876  
 DB 281 LIN----FIFLNVIRIIMTKLRASSTTSETIQYKRAVKATLVLLPLLGITYMLFFVNPGE 336  
 QY 877 ---VNVTFMVLFAINTLOGFFIFEIFYCV-----AKENVKQWRRY 914  
 DB 337 DEYSRVVVFIFNSFLESFGQFFVSVFYCLNSSEVRSAIRKRRWR 381

RESULT 12  
 ID PACR\_BOVIN STANDARD; PRT; 513 AA.  
 AC Q29627;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE pituitary adenylate cyclase activating polypeptide type I receptor  
 DE precursor (PACAP type I receptor) (PACAP-R-1).  
 DDE ADCVAP1RL.  
 3N Bos taurus (Bovine).  
 3S Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 3C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 3C Bovidae; Bovinae; Bos.  
 3X NCBI\_TaxID=9913;  
 3X [1]  
 3N SEQUENCE FROM N.A.  
 3P TISSUE=Brain;

RX MEDLINE-94325336; PubMed-8049255;  
 RA Miyamoto Y., Habata Y., Ohtaki T., Masuda Y., Ogi K., Onda H.,  
 RA Fujino M.;  
 RT "Cloning and expression of a complementary DNA encoding the bovine  
 RT receptor for pituitary adenylate cyclase-activating polypeptide  
 RT (PACAP).";  
 RL Biochim. Biophys. Acta 1218:297-307(1994).  
 CC -I- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE  
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
 CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,  
 CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND  
 CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM  
 CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE  
 CC GASTROINTESTINAL TRACT (BY SIMILARITY).  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM (SHOWN  
 CC HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -I- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; D17290; BAA04122.1; -;  
 CC EMBL; D17290; BAA04123.1; -;  
 CC GCRDB; GCR\_2658; -;  
 CC GCRDB; GCR\_2659; -;  
 CC InterPro; IPR000832; GPCR\_secretin.  
 CC InterPro; IPR001879; hormn\_receptor.  
 CC Pfam; PF00002; 7tm\_2; 1.  
 CC Pfam; PF02793; HRM; 1.  
 CC PRINTS; PR00249; GPCRSECRETIN.  
 CC SMART; SM00008; HORMR; 1.  
 CC PROSITE; PS00649; G-PROTEIN\_RECP\_F2\_1; 1.  
 CC PROSITE; PS00650; G-PROTEIN\_RECP\_F2\_2; 1.  
 CC PROSITE; PS02227; G-PROTEIN\_RECP\_F2\_3; 1.  
 CC PROSITE; PS02661; G-PROTEIN\_RECP\_F2\_4; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 37  
 FT CHAIN 38 513  
 FT  
 FT PITUITARY ADENYLATE CYCLASE ACTIVATING  
 FT POLYPEPTIDE TYPE I RECEPTOR.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT 1 (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT 2 (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT 3 (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT 4 (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT 5 (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT 6 (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT 7 (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 65 65  
 FT CARBOHYD 77 77  
 FT CARBOHYD 134 134  
 FT VARSPLIC 366 393  
 FT SEQUENCE 513 AA; 58785 MW; 9A45753210CE9817 CRC64;  
 Query Match 4.3%; Score 228.5; DB 1; Length 513;  
 Best Local Similarity 21.5%; Pred. No. 2.6e-05;  
 Matches 107; Conservative 89; Mismatches 164; Indels 137; Gaps 25;

[illegible]

QY 755 YILKFCIVGSGVPAVVTIILTISP--DNYGLSGYKFPNGSPDDFCWINNN--AVFYI- 809  
 Db 265 YFYWYTIIGTPTVCTVWATLRLYFDGTG-----CWDNDSTALMWVI 309  
 QY 810 --TVVGYFCVIFLLNVSMFVVLVOLCRKKKOLGAORKTSTQDLRSIAGLTFLLGITW 867  
 Db 310 KGPVGSIMVNFVFIGI-IVILVO--KLQSPDMGNGESSIYLRSLRLLIPLIFGI-- 364  
 QY 868 GFAFFAGWPVNVV--FMYLEAI-ENTLQGFIFIFYCV-----AKENVKQWRYYLCCGKL 920  
 Db 365 HYTVFAFSPENVKRRLVPELGLSGSQGFVVAVLYCFELNGEVAEIKRKRWSKYNRYF 424  
 QY 921 RLAEKSDSKATNGLKQVNVQGVSSSSSSLOSS 955  
 Db 425 AVDFKRRHPSLASSGVNGGTQLSTLSKSSQIRMS 459  
 RESULT 14  
 ID CRFL\_MOUSE STANDARD; PRT; 415 AA.  
 AC P35347;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)  
 DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).  
 GN CRHR1 OR CRHR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=pituitary;  
 RX MEDLINE=94063063; PubMed=8243652;  
 RA Vita M., Laurent P., Lefort S., Chalou P., Lelias J.-M., Kachad M.,  
 le Fur G., Caput D., Ferrara P.;  
 RT "Primary structure and functional expression of mouse pituitary and  
 human brain corticotropin releasing factor receptors.";  
 RL FEBS Lett. 335:1-5(1993).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.  
 CC SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS  
 CC MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL CYCLASE.  
 CC -!- TISSUE SPECIFICITY: Integral membrane protein.  
 CC -!- SUBCELLULAR LOCATION: BRAIN, PITUITARY GLAND, TESTIS. NOT DETECTED  
 CC IN PLACENTA, PERIPHERAL BLOOD, LYMPHOCYTES, KIDNEY AND LIVER.  
 CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL: X72305; CAA51053.1; -  
 CC PIR: S39535; S39535.  
 CC GCRD: GCR\_0848; -  
 CC MGD: MGI:88498; Crhr.  
 CC InterPro: IPR000832; GPCR\_secretin.  
 CC IntraPro: IPR001879; hormn\_receptor.  
 CC Pfam: PF00002; 7tm\_2; 1.  
 CC Pfam: PF02793; HRM; 1.  
 CC PRINTS: PR00249; GPCRSECRETIN.  
 CC SMART: SM00008; Hormr; 1.  
 CC PROSITE: PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
 CC PROSITE: PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 CC PROSITE: PS00650; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 CC PROSITE: PS00650; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 CC PROSITE: PS00650; G\_PROTEIN\_RECEP\_F2\_5; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

KW Phosphorylation.  
 FT SIGNAL 1 24  
 FT CHAIN 25 415  
 FT 1.  
 FT DOMAIN 25 121  
 FT TRANSMEM 122 142  
 FT DOMAIN 143 151  
 FT TRANSMEM 152 171  
 FT DOMAIN 172 189  
 FT TRANSMEM 190 213  
 FT DOMAIN 214 227  
 FT TRANSMEM 228 249  
 FT DOMAIN 250 268  
 FT TRANSMEM 269 291  
 FT DOMAIN 292 314  
 FT TRANSMEM 315 334  
 FT DOMAIN 335 349  
 FT TRANSMEM 350 369  
 FT DOMAIN 370 415  
 FT CARBOHYD 38 38  
 FT CARBOHYD 45 45  
 FT CARBOHYD 78 78  
 FT CARBOHYD 90 90  
 FT CARBOHYD 98 98  
 SQ SEQUENCE 415 AA; 47769 MW; 814238DA6DICA070 CRC64;  
 Query Match 4.2%; Score 225; DB 1; Length 415;  
 Best Local Similarity 25.2%; Pred. No. 3e-05;  
 Matches 102; Conservative 70; Mismatches 151; Indels 82; Gaps 22;  
 QY 543 QDPSLENLSLISVISSVANLTVRLTVTVTLKHLNPSODELTVR-C-----VFWD 595  
 Db 26 QQQCESLSL-----ASNVSGLQC-NASVDLIGTCWPRSPA-GQLVVRPCPAFFYGVYN 78  
 QY 596 LGRNGR-----GGWSDNGCSVKDRRLNETICTCSHLTSFGVLLDLSTSVLPAAOMALT 650  
 Db 79 TNNGYRECLANGSWA-----ARVYSECC-----EILNEKKSKVHYHIAVI- 121  
 QY 651 FITYGCGLSLSPFLSVTLVTVYIAFEKIR--RDYPSKILQICALLLLNLV-FLDLSWIA 707  
 Db 122 -INLGHICSLVALLVAFVFLRLRLSIRCLRNI---IHWNIISAFILRNATFEVVLTVS 177  
 QY 708 LYKMO---GLCTISVAVFLHYFLVSVFTWGLFAHMYLALVKVENT-YIRKILKFCIVG 763  
 Db 178 PEVHQSNAVCLRVTAAYNYFHVNFWMGEGCYLHTAIVLTSTDLRKLWM--FVCIIG 235  
 QY 764 WGV--PAVVVTIILTISPNDYGLSGYKFPNGSPDDFCWINNNAVFYITVV--GYFCVIF 819  
 Db 236 WGVFPPIIWAIGLYYDN-----EKCFGKRPVYTDYIYQGPMLVL 280  
 QY 820 LLNVSMETVVLQCRIRKKKQLGAORKTSTQDLRSIAGLTFLLGITWGAFFANGP 876  
 Db 281 LIN----FIFLNFVIRLMTKLRASTSTSETIQYRKAVKATLVLLPLLGITYMLFFVNFGE 336  
 QY 877 ---VNVTFMFLFAIFNTLQGFIFIFYCV-----AKENVKQWRYY 914  
 Db 337 DEVSRVVFYFNSFLESFGGFEVSVFYCYFLNSEVRSAIRKRWRW 381  
 RESULT 15  
 ID VIPR\_RAT  
 AC P30083;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)  
 DE (Pituitary adenylate cyclase activating polypeptide type II receptor)  
 DE (PACAP type II receptor) (PACAP-R-2).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=9223232309; PubMed=1314625;  
 RA Ishihara T., Shigemoto R., Mori K., Takahashi K., Nagata S.;  
 RT "Functional expression and tissue distribution of a novel receptor  
 for vasopressin in the rat brain."  
 RL Neuron 8:811-819(1992).  
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS  
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE  
 CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: IN LIVER, LUNG, INTESTINES, THYMUS AND BRAIN  
 (MOSTLY IN THE CEREBRAL CORTEX AND HIPPOCAMPUS).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC  
 CC  
 CC EMBL; M86835; AAA42331.1; -;  
 DR PIR; JH0594; JH0594.  
 DR GCRDB; GCR\_0369; -;  
 DR InterPro; IPR000832; GPCR\_secretin.  
 DR InterPro; IPR001879; hormn\_receptor.  
 DR Pfam; PF00002; 7tm.2; 1.  
 DR Pfam; PF02793; HRM; 1.  
 DR PRINTS; PR00249; GPCRSECRETIN.  
 DR SMART; SM00008; HORMR; 1.  
 DR PROSITE; PS00649; G-PROTEIN\_RECEP\_F2.1; 1.  
 DR PROSITE; PS00650; G-PROTEIN\_RECEP\_F2.2; 1.  
 DR PROSITE; PS00651; G-PROTEIN\_RECEP\_F2.3; 1.  
 DR PROSITE; PS00652; G-PROTEIN\_RECEP\_F2.4; 1.  
 DR PROSITE; PS00653; G-PROTEIN\_RECEP\_F2.5; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 459  
 FT VASOACTIVE INTESTINAL POLYPEPTIDE  
 FT RECEPTOR 1.  
 FT DOMAIN 31 143  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 144 168  
 FT TRANSMEM 169 175  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 176 195  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 196 217  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 218 241  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 242 255  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 256 277  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 294  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 295 318  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 319 343  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 344 363  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 364 375  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 376 395  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 396 459  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 58 58  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 69 69  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 100 100  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 292 292  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 459 AA; 52057 MW; 99E8957DA86698D2 CRC64;  
 Query Match 4.2%; Score 223.5; DB 1; Length 459;  
 Best Local Similarity 23.0%; Pred. No. 4.2e-05;  
 Matches 94; Conservative 68; Mismatches 163; Indels 83; Gaps 16;  
 QY 594 WDLGRNGRGGRGSD-----NCGSKVDRRLNETICTCSHLTSFGLVLDLGRTSVLPQAM 646  
 DB 99 YNISRCTEGSQLEPGPHIACGLND-----RASSLDEQ 135

QY 647 MALTFTFY-----IGCGSSIFSLVTLYTIAFEKIR--RDYPSKILQICLAALLNLV 699  
 DB 136 QTFYNTVKYTYTIGYSLSLASLLVAMAILSLFRKLCRTNVIHMLFM--SFILRATAV 193  
 QY 700 FLDSWIALYKMOGL-----CISVAVELHYELLYSFTWGLEAFHMYLALVKVENT 750  
 DB 194 FKID--MALFNSGEIDHCSEASVGCCKAAVFFQYCVMANFFWLLVEGLYLYTLVLSFFS 251  
 QY 751 YIRKYLKFCIVGKGVPAVVVTI--ILRISPDNYGLGSKYCKPNSGPDPCW--INNNAV 806  
 DB 252 E-RKFFWGYLLIGMGVPSVFTITWTVRIYFEDFG-----CWDITINSSL 295  
 QY 807 FYITVVGVCVIFLLNVSMFIVLVOLCRKKKOLGAORQKTSIQDLRSITAGTLFLGIT 866  
 DB 296 WWI--IKAPILLSILNVFLVFCIIRILVQKLRPPDGI---KNDSSPSYSLAKSTLLDPL 351  
 QY 867 WG--FAFANGPVNV---TFMYLFALENTLOGFFIFCYCV-----AKENVKRWKRRWLQ 411  
 DB 352 FGIHYVMAFFPDNFKAQVKMVFELVVGSGFVVAIIYCFLNGEVAELRRKRRWLQ 411  
 QY 918 GKRLAENSDWSKTATNGLKQTVNQGVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 965  
 DB 412 GVLGSSKSOHPGWSNGATCTQVSMLTRVSPSARRSSSFQAEVSLV 459  
 RESULT 16  
 ID MTHL\_DROME STANDARD; PRT; 676 AA.  
 AC Q9VXD9;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Probable G-protein-coupled receptor Mth-like 1 precursor (Methuselah-  
 like 1 protein).  
 DE MTHL1 OR CG4521.  
 GN Drosophila melanogaster (Fruit fly).  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch L., Beasley E.M.,  
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Bolshakov S.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter A., Chandra I.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Davies P.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,





RESULT 18  
DIHR\_MANSE  
AC P35464; STANDARD; PRT; 395 AA.  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Diuretic hormone receptor (DH-R).  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.  
OX NCBI\_Taxid=7130;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94103310; PubMed=8276884;  
RA Reagan J.D.;  
RT "Expression cloning of an insect diuretic hormone receptor. A member  
of the calcitonin/secretin receptor family.";  
RL J. Biol. Chem. 269:9-12(1994).  
CC -!- FUNCTION: RECEPTOR FOR THE INSECT DIURECTIC HORMONE. THE ACTIVITY  
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE  
CYCLASE.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MALPIGHIAN TUBULES.  
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: U03489; AAC46469.1; -.  
DR GCRdb; GCR 0644; -.  
DR InterPro; IPR000832; GPCR\_secretin.  
DR InterPro; IPR001879; hormo\_receptor.  
DR Pfam; PF00002; 7tm\_2; 1.  
DR Pfam; PF02793; HRM; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR SMART; SM00008; HORMR; 1.  
DR PROSITE; PS00649; G\_PROTEIN\_RECP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECP\_F2\_2; 1.  
DR PROSITE; PS00651; G\_PROTEIN\_RECP\_F2\_3; 1.  
DR PROSITE; PS00652; G\_PROTEIN\_RECP\_F2\_4; 1.  
DR PROSITE; PS00653; G\_PROTEIN\_RECP\_F2\_5; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
FT DOMAIN 1 87 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 88 111 1 (POTENTIAL).  
FT DOMAIN 112 119 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 120 140 2 (POTENTIAL).  
FT DOMAIN 141 155 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 156 176 3 (POTENTIAL).  
FT DOMAIN 177 195 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 196 217 4 (POTENTIAL).  
FT DOMAIN 218 248 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 249 272 5 (POTENTIAL).  
FT DOMAIN 273 295 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 296 314 6 (POTENTIAL).  
FT DOMAIN 315 329 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 330 349 7 (POTENTIAL).  
FT DOMAIN 350 395 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 395 AA; 45420 MW; 3F8C1A3EFA01B2D CRC64;

Query Match 4.1%; Score 219; DB 1; Length 395;  
Best Local Similarity 25.6%; Pred. No. 6e-05;  
Matches 87; Conservative 62; Mismatches 117; Indels 74; Gaps 21;  
QY 643 PAOMMALTEITYICGLSSIFLSVTLVYIAFEKIR-----RDYPSKILIOICALLL 695  
Db 82 PTDVASLIYLA--GYSLAVLSLAVFVFLYFKDRLCLRNTHTNLMSTYLSACS--WI 137  
QY 696 LNLVFLDLSWI--ALYKMOGLCTISVAVFLHYFLVLLVFTWMLGFAFMALVLYKVF--NTY 751  
Db 138 LNLV--LQNSDESQDQTSMLVICHNYFYLTNFFMVLVECLYLYMLVVEFTAENIK 195  
QY 752 IRKYLKFCIVGWGPVAVVVI-----ILTISPNYGLSGYKPPNGSPDDFC--WINNN 804  
Db 196 LKVI-----TTIGWGAFAVITWISRCFVNVLPST--GPDGLAMFPEAK---MCIWMHEH 247  
QY 805 AVEFYI-----TWVGYFCVIFLLNVSFIVVLVOLCRHKKKKOLGAORKTSTQDLRSIAGLT 860  
Db 248 QVDWIHKAPALVGLALNLFLLIRIMW--VLTKLRASANTLETEQYRKAT----KALLVLI 301  
QY 861 FILGIT-----WGFAFWGPNVNTFMYLFAIFNTLQGGFFIFIFCYVAKENVR 908  
Db 302 PLLGITNLLVLCGSDSDSW--PAY-----AFDYTRALMLSTQGTVALFYCFMTEVR 352  
QY 909 -----KOWR--RYLCCGKLRLAENS--DWS--KTATNGLK 937  
Db 353 HATRYHVERWKTGTIGGRRRGASYSKDWSPRSRTESIR 392  
RESULT 19  
CRFL\_HUMAN  
ID CRFL\_HUMAN STANDARD; PRT; 444 AA.  
AC P34598; Q13008; Q9UK64;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Corticotropin-releasing factor receptor 1 precursor (CRF-R) (CRFL)  
DE Corticotropin-releasing hormone receptor 1 (CRH-R 1).  
GN CRHR1 OR CRHR OR CRFR.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=pituitary;  
RX MEDLINE=94022296; PubMed=7692441;  
RA Chen R., Lewis K.A., Perrin M.H., Vale W.W.;  
RT "Expression cloning of a human corticotropin-releasing-factor  
receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:8967-8971(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=94063063; PubMed=8243652;  
RA Vita N., Laurent P., Lefort S., Chalon P., Lelias J.-M., Kaghad M.,  
le Fur G., Caput D., Ferrara P.;  
RT "Primary structure and functional expression of mouse pituitary and  
human brain corticotropin releasing factor receptors.";  
RL FEBS Lett. 335:1-5(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Sakai K., Yamada M., Horiba N., Wakui M., Demura H., Suda T.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM CRF-R3).  
RC TISSUE=Hippocampus;  
RX MEDLINE=95110332; PubMed=7811272;  
RA Ross P.C., Kostas C.M., Ramabhadran T.V.;  
RT "A variant of the human corticotropin-releasing factor (CRF)  
receptor: cloning, expression and pharmacology.";  
RL Biochem. Biophys. Res. Commun. 205:1836-1842(1994).







TRANSMEM 169  
 DOMAIN 189  
 TRANSMEM 205  
 TRANSMEM 229  
 DOMAIN 230  
 TRANSMEM 243  
 TRANSMEM 244  
 TRANSMEM 266  
 TRANSMEM 285  
 TRANSMEM 308  
 TRANSMEM 331  
 TRANSMEM 351  
 TRANSMEM 366  
 TRANSMEM 385  
 TRANSMEM 431  
 CARBOHYD 52  
 CARBOHYD 61  
 CARBOHYD 94  
 CARBOHYD 106  
 CARBOHYD 114  
 CARBOHYD 114  
 CONFLICT 3  
 CONFLICT 126  
 CONFLICT 392  
 CONFLICT 396  
 CONFLICT 408  
 CONFLICT 431  
 SEQUENCE 431 AA; 49923 MW; A6D9EDE575DB8061 CRC64;

Query Match 3.9%; Score 208; DB 1; Length 431;  
 Best Local Similarity 24.3%; Pred. No. 0.00026;  
 Matches 68; Conservative 55; Mismatches 119; Indels 38; Gaps 12;

QY 652 ITYIGGLSIFSLVTLTYIAFEKTRDYPYSKILLQCAALLNLFVLDSTWALYKM 711  
 DB 139 VNYLGHCVSVVALVAFLFLVLRSL-RCLRNHNWLNITFTFLNIAWFLQLDIEVH 197  
 QY 712 QG---LCISVAVFLHYFLVLSFTWGLFAHMYALVAVKENT-YIRKYLKFCIVGVGPV 767  
 DB 198 EGNEWCRCITIFNVFVNTFFWFEVGCYLHTAIVMTYSTEHLRWL--FLFIGWIP 255  
 QY 768 AVVTIILITSPDNYGLSGYKFPNGSPDFCWINNA---VFYITVGVPCVIFLLNVS 824  
 DB 256 CPII-IAWAGKLYI-----ENEQCWFGKAGDLVDYI-YQGPVMLVLLIN-- 299  
 QY 825 MFIVVLVOLCRKIKKQLCAORKTSTIODLRSTAG---LTLFLIGTWGFAPFANGP---VN 878  
 DB 300 --FVFLNIVILMTKLRASITSETIYQKAVKATVLLPLLGITYMLFFVNPGEEDLSQ 357  
 QY 879 VTFMYLFAFNLTQGFIFIFVYV---AKENVRKQWRY 914  
 DB 358 IVFIYNSFLQSFQGFVSVFYCFENGVEVRAALRKRWHRW 397  
 [1]

RESULT 23  
 VIPR\_HUMAN  
 ID VIPR\_HUMAN STANDARD; PRT; 457 AA.  
 AC P32241; Q15871;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)  
 DE (Pituitary adenylate cyclase activating polypeptide type II receptor)  
 DE (PACAP type II receptor) (PACAP-R-2).  
 GN VIPR1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Intestine;  
 RX MEDLINE=93290641; PubMed=8390245;  
 RA Sreedharan S.P., Patel D.R., Huang J.-X., Goetzl E.J.;  
 RT "Cloning and functional expression of a human neuroendocrine  
 RT vasoactive intestinal peptide receptor."  
 RL Biochem. Biophys. Res. Commun. 193:546-553(1993).

RN [2]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Intestine;  
 RX MEDLINE=94235025; PubMed=8179610;  
 RA Couvineau A., Rouyer-Fessard C., Darmoul D., Maoret J.J., Carrero I.,  
 RA Ogier-Denis E., Laburthe M.;  
 RT "Human intestinal VIP receptor: cloning and functional expression of  
 RT two cDNA encoding proteins with different N-terminal domains.";  
 RL Biochem. Biophys. Res. Commun. 200:769-776(1994).  
 RP [3]  
 RP SEQUENCE OF 33-457 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=95001220; PubMed=7917790;  
 RA Gagnon A.W., Aiyar N., Elshourbagy N.A.;  
 RT "Molecular cloning and functional characterization of a human liver  
 RT vasoactive intestinal peptide receptor.";  
 RL Cell. Signal. 6:321-333(1994).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS  
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL  
 CC CYCLASE. THE AFFINITY IS VIP = PACAP-27 > PACAP-38.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -!- TISSUE SPECIFICITY: IN LUNG, HT29 COLONIC EPITHELIAL CELLS,  
 CC RAJI B-LYMPHOBLASTS. LESSER EXTENT IN BRAIN, HEART, KIDNEY,  
 CC LIVER AND PLACENTA.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 CC EMBL; U11087; AAB60362.1; JOINED.  
 CC EMBL; U11079; AAB60362.1; JOINED.  
 CC EMBL; U11080; AAB60362.1; JOINED.  
 CC EMBL; U11081; AAB60362.1; JOINED.  
 CC EMBL; U11083; AAB60362.1; JOINED.  
 CC EMBL; U11084; AAB60362.1; JOINED.  
 CC EMBL; U11085; AAB60362.1; JOINED.  
 CC EMBL; U11086; AAB60362.1; JOINED.  
 CC EMBL; L13288; AAA36805.1; JOINED.  
 CC EMBL; X77777; CAA54814.1; JOINED.  
 CC EMBL; X75299; CAA53046.1; JOINED.  
 CC EMBL; L20295; AAA36802.1; JOINED.  
 CC PIR; JN0604; JN0604.  
 CC GCRDB; GCR\_0397; -.  
 CC GCRDB; GCR\_0652; -.  
 CC GCRDB; GCR\_0774; -.  
 CC GCRDB; GCR\_0904; -.  
 CC GCRDB; GCR\_1888; -.  
 CC MIM; 192321; -.  
 CC InterPro; IPR000832; GPCR\_secretin.  
 CC InterPro; IPR001879; hormn\_receptor.  
 CC Pfam; PF00002; 7tm.2; 1.  
 CC Pfam; PF02793; HRM; 1.  
 CC PRINTS; PR00249; GPCRSECRETIN.  
 CC SMART; SM00008; Hormr; 1.  
 CC PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
 CC PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 CC PROSITE; PS00651; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 CC PROSITE; PS00652; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 CC PROSITE; PS00653; G\_PROTEIN\_RECEP\_F2\_5; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 CC Alternative splicing.  
 CC SIGNAL 1 30  
 CC CHAIN 31 457  
 CC  
 CC POTENTIAL.  
 CC VASOACTIVE INTESTINAL POLYPEPTIDE  
 CC RECEPTOR 1.  
 CC  
 CC DOMAIN 31 142  
 CC TRANSMEM 143 167  
 CC DOMAIN 168 174  
 CC  
 CC EXTRACELLULAR (POTENTIAL).  
 CC 1 (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	175	194	2 (POTENTIAL).
FT	DOMAIN	195	216	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	217	240	3 (POTENTIAL).
FT	DOMAIN	241	254	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	255	276	4 (POTENTIAL).
FT	DOMAIN	277	292	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	293	316	5 (POTENTIAL).
FT	DOMAIN	317	341	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	342	361	6 (POTENTIAL).
FT	DOMAIN	362	373	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	374	393	7 (POTENTIAL).
FT	DOMAIN	394	457	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	58	58	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	69	69	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	100	100	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPLIC	1	32	MRPSPPLPMMWGLVSLALAWALGPGAGGAAR > MPPPP
FT				LLLSRRRLGGGSVATRLVVVAAGARSRRGGGSGRAGGGGR
FT				GGVARRRRLCSFSECAILLGSS (IN LONG ISOFORM).
FT	SEQUENCE	457 AA;	51547 MW;	DAAA00CF5BEC47D7D CRC64;
SO				

Query Match 3.9%; Score 208; DB 1; Length 457;  
Best Local Similarity 24.1%; Pred. No. 0.00028;  
Matches 94; Conservative 55; Mismatches 167; Indels 74; Gaps

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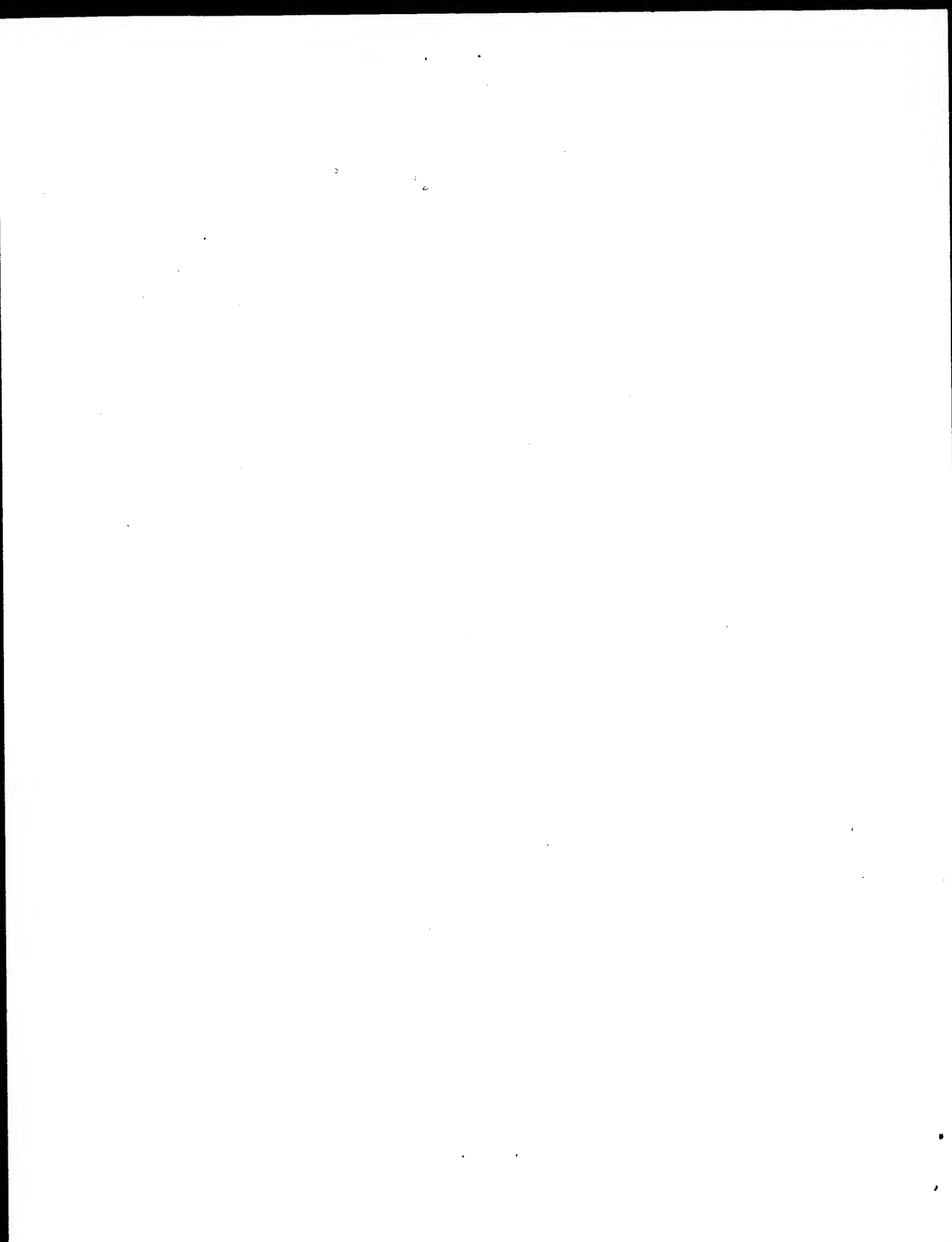
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||| |||
98 GNVRSCSTDGWHLEPGPYPIACGLDDKAAS-----LDEQQTMYGVSV 142
||| |||
645 MMALPFIYIGCCLSSEIFLSVLTVYIAFEKIR--RDYPSK-----ILIQCAALLLLNVF 700
||| |||
143 KTYGT-----IGYGLSLATLLVATAILSLFPKLHCTRTNIIMHUIPISILRAAVFIKDLA 198
||| |||
701 LLDSSWIALYKMOGL--CISVAVLHFLVSWFTWMGLEAFHMYLALVKVFNTYIRKYILK 758
||| |||
199 LFDGSGDQCSGSEGVCKAAWVFQYCVMANFFWLLVEGLYLYTLTLLAVSFSE-RKYFWG 257
||| |||
759 FCIVGKGVPA--VVVTHIITSPDNYGLSGYKFPNGPPDDFCWINNNAVITYTVWGVC 816
||| |||
258 YILIGWGPSTFTMWVTTIARHFEYD-----CWDTINSSLIWWTIKGPIL 302
||| |||
817 VIFLLNMFPIVVLVOLCRKKKKQJLGAQRKSTQDRLSRTAGLFLGLITWG--FAFPAW 874
||| |||
303 TSLVNFPIFCIIRILLQKLRPDI---RKSDSPYSRLARSTLLLLPLEGVHIYHFAF 359
||| |||
875 GPVNV---TFMYLFAINTLQGFPEFIYFCV---AKENVKRWRRYILCCGLKLAENSD 927
||| |||
360 FPDNFKPEVKMVELVVGVSFGFVVAIYCLFNGEVAELRRKKRRWHLQGVLGWNPYR 419
||| |||
928 WSKTATNGLKKQT-----VNGCVSSSN 950
||| |||
420 HPSGGNGATCSTQVSMLTRVSPCARSSS 449
||| |||

```

RESULT	24	SCRC_RABIT	SCRC_RABIT	STANDARD;	PRT;	445 AA.
ID						
AC						O46502;
DT						15-JUL-1999 (Rel. 38, Created)
DT						15-JUL-1999 (Rel. 38, Last sequence update)
DT						16-OCT-2001 (Rel. 40, Last annotation update)
DE						Serotonin receptor precursor (SCT-R).
GN						SCTR.
OS						Oryctolagus cuniculus (Rabbit).
OC						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC						Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX						NCBI_TaxID=9986;
RN						[1]
RN						SEQUENCE FROM N.A.
RP						MEDLINE=98366112; PubMed=9700755;
RX						Svoboda M., Tاستنوي M., de Neef P., Delporte C., Waelbroeck M.,
RA						Robberecht P.;
RA						

EMBL; L41563; AAA96656.1;	-
GCRdb; GCR_1l80;	-
InterPro; IPR000832;	GPCR_secretin.
InterPro; IPR001879;	hornm_receptor.
Pfam; PF00002; 7tm_2;	1.
Pfam; PF02793; HRM;	1.
PRINTS; PR00249;	GPCRSECRETIN.
SMART; SM00008;	Hormr; 1.
PROSITE; PS00649;	G_PROTEIN_RECEP_F2.1; 1.
PROSITE; PS00650;	G_PROTEIN_RECEP_F2.2; 1.
PROSITE; PS50227;	G_PROTEIN_RECEP_F2.3; 1.
PROSITE; PS50261;	G_PROTEIN_RECEP_F2.4; 1.
G-protein coupled receptor; Transmembrane;	Glycoprotein; Signal.
SIGNAL	1 28
CHAIN	29 420
	CORTICOTROPIN RELEASING FACTOR RECEPTOR 1.
DOMAIN	29 126
TRANSMEM	127 147
FT	1 (POTENTIAL).
DOMAIN	EXTRACELLULAR (POTENTIAL).
TRANSMEM	148 156
FT	CYTOPLASMIC (POTENTIAL).
DOMAIN	157 176
FT	2 (POTENTIAL).
DOMAIN	177 194
FT	EXTRACELLULAR (POTENTIAL).
TRANSMEM	195 218
FT	3 (POTENTIAL).
DOMAIN	219 232
FT	CYTOPLASMIC (POTENTIAL).
TRANSMEM	233 254
FT	4 (POTENTIAL).

Search completed: May 23, 2002, 07:39:47  
Job time: 166 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 23, 2002, 07:35:41 ; Search time 40.63 seconds  
(without alignments)  
4419.610 Million cell updates/sec

Title: US-09-731-657-2

Perfect score: 5352

Sequence: 1 SQPEDASGRCAQRFSTLFE.....GRMALRRTSKRGLHFTQEM 1038

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5232	97.8	1014	4	O00406
2	1372.5	25.6	512	4	O96JW0
3	1368.5	25.6	541	4	O9Y3K0
4	651.5	12.2	687	11	O902H2
5	629	11.8	687	4	O95966
6	618	11.5	693	4	O96HB4
7	617.5	11.5	693	4	O9Y653
8	589	11.0	823	4	O90HX3
9	539	10.1	1403	4	O95490
10	536.5	10.0	1283	6	O97823
11	536.5	10.0	1351	6	O97829
12	536.5	10.0	1512	6	O97821
13	536.5	10.0	1580	6	O97821
14	536	10.0	1527	11	O88927
15	534	10.0	1274	6	O97820
16	534	10.0	1342	6	O97826

17	534	10.0	1450	6	O97811	O97811 bos taurus
18	534	10.0	1503	6	O97818	O97818 bos taurus
19	534	10.0	1571	6	O97824	O97824 bos taurus
20	533.5	10.0	1240	6	O97822	O97822 bos taurus
21	533.5	10.0	1308	6	O97828	O97828 bos taurus
22	533	10.0	872	4	O94867	O94867 homo sapien
23	531.5	9.9	1407	6	O97810	O97810 bos taurus
24	531.5	9.9	1550	11	O92173	O92173 rattus norv
25	531	9.9	1231	6	O97819	O97819 bos taurus
26	531	9.9	1299	6	O97825	O97825 bos taurus
27	530.5	9.9	1177	4	O9UKY6	O9UKY6 homo sapien
28	530	9.9	1021	4	O94882	O94882 homo sapien
29	528.5	9.9	1465	6	O97813	O97813 bos taurus
30	527.5	9.9	1463	6	O97815	O97815 bos taurus
31	526	9.8	1240	4	O9HAR2	O9HAR2 homo sapien
32	526	9.8	1422	6	O97812	O97812 bos taurus
33	525	9.8	1420	6	O97814	O97814 bos taurus
34	522	9.8	1123	4	O9UKY5	O9UKY5 homo sapien
35	522	9.8	1478	6	O97817	O97817 bos taurus
36	520.5	9.7	1384	6	O97803	O97803 bos taurus
37	519.5	9.7	1435	6	O97816	O97816 bos taurus
38	518	9.7	1341	6	O97802	O97802 bos taurus
39	517	9.7	1449	5	O10922	O10922 caenorhabdi
40	515	9.6	1399	6	O97805	O97805 bos taurus
41	514	9.6	1397	6	O97807	O97807 bos taurus
42	512.5	9.6	1356	6	O97804	O97804 bos taurus
43	511.5	9.6	1354	6	O97806	O97806 bos taurus
44	508.5	9.5	1412	6	O97809	O97809 bos taurus
45	507.5	9.5	986	5	O9N9W3	O9N9W3 haemochus
46	506.5	9.5	2144	11	O9QYF2	O9QYF2 rattus norv
47	506	9.5	1369	6	O97808	O97808 bos taurus
48	505	9.4	1467	6	O97830	O97830 bos taurus
49	505	9.4	1472	6	O97831	O97831 bos taurus
50	503.5	9.4	1469	4	O9HAR3	O9HAR3 homo sapien
51	503.5	9.4	1474	4	O94910	O94910 homo sapien
52	501.5	9.4	652	4	O9BY15	O9BY15 homo sapien
53	500.5	9.4	1478	11	O88923	O88923 rattus norv
54	498	9.3	1487	11	O92174	O92174 rattus norv
55	495.5	9.3	2920	11	O9F0M0	O9F0M0 mus musculus
56	494	9.2	1515	11	O88917	O88917 rattus norv
57	494	9.2	2408	4	O92566	O92566 homo sapien
58	494	9.2	2923	4	O9HCU4	O9HCU4 homo sapien
59	493.5	9.2	732	6	O95162	O95162 sus scrofa
60	491.5	9.2	835	4	O00718	O00718 homo sapien
61	489	9.1	899	11	O9K26	O9K26 mus musculus
62	476.5	8.9	738	11	O91W44	O91W44 mus musculus
63	472	8.8	722	11	O9DC42	O9DC42 mus musculus
64	472	8.8	724	11	O923A1	O923A1 mus musculus
65	471.5	8.8	986	4	O94858	O94858 homo sapien
66	471	8.8	884	11	O922R4	O922R4 mus musculus
67	470.5	8.8	1346	4	O9U1Z3	O9U1Z3 homo sapien
68	468	8.7	1318	4	O9H1S2	O9H1S2 homo sapien
69	467	8.7	724	11	O9JLQ8	O9JLQ8 mus musculus
70	467	8.7	739	11	O923X1	O923X1 mus musculus
71	463.5	8.7	999	4	O9H1S1	O9H1S1 homo sapien
72	463	8.7	344	4	O9Y4B1	O9Y4B1 homo sapien
73	463	8.7	738	11	O9ESC1	O9ESC1 rattus norv
74	462.5	8.6	797	4	O9K78	O9K78 homo sapien
75	462	8.6	818	11	O9Z0M6	O9Z0M6 mus musculus
76	459.5	8.6	1092	4	O9H1S4	O9H1S4 homo sapien
77	458	8.6	606	4	O9HBW9	O9HBW9 homo sapien
78	457.5	8.5	839	4	O96IE7	O96IE7 homo sapien
79	457	8.5	689	11	O91ZE5	O91ZE5 mus musculus
80	457	8.5	3034	4	O35161	O35161 mus musculus
81	452	8.4	1014	5	O17505	O17505 caenorhabdi
82	451	8.4	1038	4	O9H1S3	O9H1S3 homo sapien
83	447	8.4	1477	4	O95722	O95722 homo sapien
84	447	8.4	3014	4	O9NYQ6	O9NYQ6 homo sapien
85	420.5	7.9	3301	11	O91Z10	O91Z10 mus musculus
86	410	7.7	1349	11	O9WVT0	O9WVT0 rattus norv
87	406	7.6	774	5	O9VA13	O9VA13 drosophila
88	405.5	7.6	3313	11	O88278	O88278 rattus norv
89	397	7.4	1364	4	O75092	O75092 homo sapien



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Db 541 TVNLRNVTVLKHNPSODELTVRCVFDLGRNGRGWSDNGCSVRDRLNETICTC 600
QY 625 SHLTSGVLLDLRTSVLPQMMALTFITYIGCGLSIFLSVTLTYIAFEKIRRDYPSK 684
Db 601 SHLTSGVLLDLRTSVLPQMMALTFITYIGCGLSIFLSVTLTYIAFEKIRRDYPSK 660
QY 685 ILIQCAALLLNLFVLLDSWIALYKMOGLCISVAVFLHYFLVFTWMLGFEAFHMYLAL 744
Db 661 ILIQCAALLLNLFVLLDSWIALYKMOGLCISVAVFLHYFLVFTWMLGFEAFHMYLAL 720
QY 745 VKVFNTYIRKYILKFCIVGCVPAVVVTIILTISPDNYGLSGYKFPNGSPDDFCWINN 804
Db 721 VKVFNTYIRKYILKFCIVGCVPAVVVTIILTISPDNYGLSGYKFPNGSPDDFCWINN 780
QY 805 AVEYITVVGFCYFVIFLLNVSMFIVLVOLCRKIKKKQLGAQRKTSIQDLRSIAGLTFLLG 864
Db 781 AVEYITVVGFCYFVIFLLNVSMFIVLVOLCRKIKKKQLGAQRKTSIQDLRSIAGLTFLLG 840
QY 865 ITWGAFFAFWANGPVNVTMYLFAFNTLOGFFIFIFYCVAKENVRKOWRRLCCGKLRLAE 924
Db 841 ITWGAFFAFWANGPVNVTMYLFAFNTLOGFFIFIFYCVAKENVRKOWRRLCCGKLRLAE 900
QY 925 NSDWSKTATNGLKQTVNGVSSSSNSLQSSNSTNTLLVNNDCSVHASNGNASTER 984
Db 901 NSDWSKTATNGLKQTVNGVSSSSNSLQSSNSTNTLLVNNDCSVHASNGNASTER 960
QY 985 NGVSFSVQNGDVCLHDFDTGKHMFNEKEDSCNGKGRMALRRTSKRGLHFIEQM 1038
Db 961 NGVSFSVQNGDVCLHDFDTGKHMFNEKEDSCNGKGRMALRRTSKRGLHFIEQM 1014

RESULT 2
Q96JW0 PRELIMINARY; PRT; 512 AA.
ID Q96JW0
AC Q96JW0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ14937 FIS, CLONE PLACE1010231, WEAKLY SIMILAR TO CELL
DE SURFACE GLYCOPROTEIN EMRI PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
RA Wadatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Takiguchi S.,
RA Takahashi M., Chiba K., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027843; BAB55406.1; -.
SQ SEQUENCE 512 AA; 57870 MW; BB4EC50BF3FCDDBE CRC64;

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Query Match 25.6%; Score 1372.5; DB 4; Length 512;  
 Best Local Similarity 52.6%; Pred. No. 2.4e-88;  
 Matches 266; Conservative 89; Mismatches 124; Indels 27; Gaps 11;

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QY 507 IGTITLPSLLMNNLPAHDMELASRVQNFETPALFDPSLENLSIYVTSVVANLTVC 566
Db 11 LASVILPNNLENLSPEDSVLVRRAGFTFNKTGLQDVGPQRKTLVSYVMACSGNITI 70
QY 567 RNLTRNVTVLKHNPSODELTVRCVFDLGRNGRGWSDNGC-SYKDRRLNETICTCS 625
Db 71 QNLKDPVOIKIKHTTQEVHHP1-CAFWDLNKNKSGFWNTSGCVAHRDSDASETVCLCN 129

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QY 626 HLTSFGVLLDLRT-SVLPAQ-MMALTFITYIGCGLSIFLSVTLTYIAFEKIRRDYPS 683
Db 130 HTHFGVLMDLPRASQDLARNTKVLTFISYIGCGISAIFSAATLLTYVAFEKLRDYP 189
QY 684 KILIQCAALLLNLFVLLDSWIALYKMOGLCISVAVFLHYFLVFTWMLGFEAFHMYLA 743
Db 190 KILMNLSTALLFNLLFDLGGWITSFNVNGLGCI-AVAVLLHFFELLATFTWMLGFEAFHMYIA 249
QY 744 LVKVFNTYIRKYILKFCIVGCVPAVVVTIILTISPDN--YGLSGYKFPNGSPDDFCWI 801
Db 250 LVKVFNTYIRRYILKFCIIIGMGLPALVSVVLASNNNEVYKESYK---EKGDFFCWI 306
QY 802 NNAVEYITVVGFCYFVIFLLNVSMFIVLVOLCRKIKKKQLGAQRKTSIQDLRSIAGLTF 861
Db 307 QDPVIFYVCAGYGVYFLLNIAMFIVVVOICGNGRGRNRTLREEVLRNLSVSLTF 366
QY 862 LLGIWGAFFAFWANGPVNVTMYLFAFNTLOGFFIFIFYCVAKENVRKOWRRLCCGKLRL 921
Db 367 LLGMTWGAFFAFWANGPLNIPMYLFSIFNSLQGLFIFIFHCAMKENVKQWRRHLCCGRPR 426
QY 922 LAENSWSKTATNGLKQTVNGVSSSSNSLQSS-----NSTNSTLLVNNDCSVHAS 975
Db 427 LADNSWSKTATNIIKSSDNLGKSLSSSGNSTYLTLSKSSSTTYFKRN-----S 480
QY 976 GNGNASTERNVGSFVQNGDV--CLH 999
Db 481 HTDNVSYEH--SFN-KSGSLRQCFH 502

RESULT 3
Q9Y3K0 PRELIMINARY; PRT; 541 AA.
ID Q9Y3K0
AC Q9Y3K0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DJ287G14.2 (PUTATIVE NOVEL SEVEN TRANSMEMBRANE DOMAIN PROTEIN)
DE (FRAGMENT).
GN DJ287G14.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mashreghi-Mohammadi M.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL033377; CAB42901.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF01825; GPS; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00303; GPS; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 541 AA; 61048 MW; 0672C54BEEC7E91D CRC64;

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Query Match 25.6%; Score 1368.5; DB 4; Length 541;  
 Best Local Similarity 52.2%; Pred. No. 4.8e-88;  
 Matches 261; Conservative 92; Mismatches 126; Indels 21; Gaps 8;

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QY 507 IGTITLPSLLMNNLPAHDMELASRVQNFETPALFDPSLENLSIYVTSVVANLTVC 566
Db 11 LASVILPNNLENLSPEDSVLVRRAGFTFNKTGLQDVGPQRKTLVSYVMACSGNITI 70
QY 567 RNLTRNVTVLKHNPSODELTVRCVFDLGRNGRGWSDNGC-SYKDRRLNETICTCS 625
Db 71 QNLKDPVOIKIKHTTQEVHHP1-CAFWDLNKNKSGFWNTSGCVAHRDSDASETVCLCN 129
QY 626 HLTSFGVLLDLRT-SVLPAQ-MMALTFITYIGCGLSIFLSVTLTYIAFEKIRRDYPS 683

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Db 130 HFTFGVMDLPRSASQDARNTKVLTFISVIGGISAIFAATLITVAEKLRRDPS 189
QY 684 KILIOCAALLNLNVLFLDSWIALYKMQGLCISAVFLHYFLVLSFTWMLGFAFMYLA 743
Db 190 KILMNSTALLFLNLLDGGWITSFNVGDLGCIADVALLHFFLLATFTWMLGFAHMYTA 249
QY 744 LKVFNTYIRKYILKFCIVGNGVAVVVTIILTSPOD--YGLSGYGFPPNGSPDDFCWI 801
Db 250 LKVFNTYIRRYILKFCIIIGWGLPALVSVVSLASNNNEVYKESYK---EKGDEFECWI 306
QY 802 NNNAVFIYVGVFCVFLNLSMFIVVLVOLCRKKKOLGAORKTSTODLRSIAGLTF 861
Db 307 QDPIEFVTCAGVGVNFFLNIAMFIVVMVQICGRNGRKSRTLREELRLNLSVSLTF 366
QY 862 LLGITGFAFFGMPVNVMTYMLFAINTLQGGFFIFCYCAKENVRKQWRYLCCGKLR 921
Db 367 LLGWTGFAFFGMPVNVMTYMLFAINTLQGGFFIFCYCAKENVRKQWRYLCCGKLR 921
QY 922 LAENSDWKTATNGLKKQTVNOGVSSSSNSLOSS-----NSTNSTLLVNDSCVHAS 975
Db 427 LAENSDWKTATNGLKKQTVNOGVSSSSNSLOSS-----NSTNSTLLVNDSCVHAS 975
QY 976 GNGNASTERNGVSPFVQNG 995
Db 481 HTDSASMDKSLSLAHADGD 500

RESULT 4
Q0Q2T2 PRELIMINARY; PRT; 687 AA.
AC Q0Q2T2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SERPENTINE RECEPTOR.
GN GPR56 OR CYT28.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=LIVER;
RA Phillips R.L., Ernst R.E., Dosil M., Wesley C.K., Moore K.A.,
RA Kingsley P.D., Sykes S., Palis J., Lemischka I.R.;
RT "Identification of novel hematopoietic stem cell regulatory genes.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF166382; AAF00617.1; -.
DR MGD; MGI:1340051; Gpr56.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm2; 1.
DR Pfam; PF01825; GPS; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00303; GPS; 1.
DR PROSITE; PS00455; AMP_BINDING; UNKNOWN_1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 687 AA; 77271 MW; B5315D70AF443809 CRC64;

Query Match 12.2%; Score 651.5; DB 11; Length 687;
Best Local Similarity 28.2%; Pred. No. 1.8e-37;
Matches 174; Conservative 118; Mismatches 258; Indels 67; Gaps 16;

QY 342 QSETISSPMPOTHVSGTPPPVKASRSPVSPAPVNTVTSAPPVQDQIVNTSSISDLENQ 401
Db 127 QSLQKQAGPLIATSVSSQWIPQNTSLP----GAPSFIFSFHNAHKVSHNASVDMCDLKE 182
QY 402 VLQWEKALSLGSLPLENLAGEMTNQVSRLLHSPDML-APLAQRLKLVDDIGLQNFNT 460

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Db 183 -----LQQLSRYLQHPQKAARKPTAAAFISQQLQSLESKL-----T 217
QY 461 TISLTSPLALAIRVNASSFNFTTFVAQDPANLOVLSLETOAPENSIGTITLTPSSLMNML 520
Db 218 SVSPLGDTLFEEDRVNATVWKLPPTAGLEDLHHSQKEEEOSEVOAYLULLPRAVFOQT 277
QY 521 PAHDMELASVOENFEETPALFQDPSLENLSLISVSSVANLTVRNLTNRNVTYTKHI 580
Db 278 RRRDDAKRLLVDFSSQALFQDKNSQV-LGEKVLGIVQNTKVTNLSDPVLTFOH- 335
QY 581 NPSDELTVCVFW-DLGRNGRGWSDNGSCVKORRLNETTCTCSHLTSFGVLLDLSRT 639
Db 336 QPQPKNTVLCVFWEDPASSTGWSAGCETVSRD-TQTSLCNHLYFAVLM-VSST 393
QY 640 SVLPAQMMALFLYIGGLSIFLSVLTVAIEKIRRDYPSKILIOCAALLNLNVL 699
Db 394 EVEATHKHYLLSVGCVISALACVFIIAALCSRRKSDYTIKVMNLLSAVFLDVS 453
QY 700 FLDSWIALYKMQGLCISAVFLHYFLVLSFTWMLGFAFMYLAHYLVNTYIRKYILKF 759
Db 454 FLLSEPVALTGSEACRTSAMFLHFSLLACTLSWMLGEGYLNLYRVVEVFGTYVPGYLLKL 513
QY 760 CIVGNGVAVVVTIILTSPOD--LGSYGKFPNG-SPDDFCWINNNAVFIYTVVGYFC 816
Db 514 SIVGNGFVFLVTLVALVDVNNYGPILAVRRTPEKTYPSMCWIRDSLSVYVTLNGLFS 573
QY 817 VIFLNVSMFTVWLVOLCRKKKOLGAORKTSTODLRSIAGLTFLLGITWGAFFAW-- 874
Db 574 LVFLNLAMLATVWVQILRLPHSQ-----NPHVLTLLGLSLVGLPMAVFFSFAS 626
QY 875 GPVNVTFMYLFAINTLQGGFFIFCYCAKENVRKQW--RRYLCCGKRLRAENSDWSKTA 932
Db 627 GTFQVLVLYLFSIITSYQGLFLWY-----WSMRFOAGQGPSPLKNNSDSACL- 675
QY 933 TNGLKQTVNOGVSSSS 949
Db 676 -----PISSGSTSSS 685

RESULT 5
Q05966 PRELIMINARY; PRT; 687 AA.
AC Q05966;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TM7XN1 PROTEIN PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99198960; PubMed=10100861;
RA Zandman A.J.W., Cornelissen I.M.H.A., Weidle U.H., Ruiter D.J.,
RA Van Muijen G.N.P.;
RT "TM7XN1, a novel human EGF-TM7 like protein, detected with mRNA
RT Differential display using human melanoma cell lines with different
RT metastatic potential.";
RL FEBS Lett. 446:292-298(1999).
DR EMBL; AJ011001; CAB37294.1; -.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm2; 1.
DR Pfam; PF01825; GPS; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00303; GPS; 1.
DR PROSITE; PS00455; AMP_BINDING; UNKNOWN_1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 25 POTENTIAL.
FT CHAIN 26 687 TM7XN1 PROTEIN.

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SQ SEQUENCE 687 AA; 77150 MW; B3F0EE75B0CD5CF1 CRC64;

Query Match 11.8%; Score 629; DB 4; Length 687;  
Best Local Similarity 28.4%; Pred. No. 7e-36;  
Matches 177; Conservative 114; Mismatches 245; Indels 88; Gaps 19;

QY 360 PPVKAS-----FSSPTVSAPANVNTTSA--PPVQTDIVNTSSISDLENQVLOMEKALSIG 412  
DB 133 PPLIATSVTSMWSPQNISLPSAASFTFSFSPHTAAHNASV-----DMCELKRDQL- 185  
QY 413 SLEPNLAGEMINQVSRLLHSP-----DMLAPLAQRLKLVVDIGLQLNFSNTTISTSP 467  
DB 186 -----LSQFLKHQKASRRPSAASQOQSLESKL-----TSVRFMGD 224  
QY 468 SLALAVIRVNASSNTTFFVAQDPANQVLSLETOAPENSIGTITLPSLMMNNLPAHDMEL 527  
DB 225 MVSEEDIRINATVWKLOPTAGLQDLHIHSRQEEQSEIMEYSVLLPRTLFQRTKGRGEA 284  
QY 528 ASRVQNFETPALFQDPSPLENLSLISYVSSVANLTVRNLTNRNVTTLKH-INPQDE 586  
DB 285 EKRLLLVDFSSQALFQDKNSSHV-LGEKVLGIWVQNTKVANLTPVVLTFQHQLOPK--N 341  
QY 587 LTVRCVFW-DLGRNGRGCGWDGSCVDRRLNETICTSHLTSFGVLLDLSRTSVLPQA 645  
DB 342 VTLCQVFWEDPTLSSPGHWSAGCETV--RRETQTSFCNHLTYFAVLM--VSSVEVDVAVH 399  
QY 646 MMALTFITYICGGLSSIFLSVTLVITYIAFEKTRRDYPSKILIOALCAALLNLVFLDLSW 705  
DB 400 KHYLSLLSYGCVVSAALACTVIAAYLCSSRPDRYTIKVMNLLAVFLDLSFLLSEP 459  
QY 706 IALYKQGLCISVAVFLHYFLVFTWGLFAFMYLALVKVFNTRYIRKYILKFCIVGWG 765  
DB 460 VALTGSAGCRASAIHFHLSLLTCLSMGLEGNLYRLVVEFGTVPGVYLLSANGWG 519  
QY 766 VPAAVVTIILTSIDPNYG--LGSYKPKPENG--SPDDFCWINNNAVFYITVVGVCVIFLLN 822  
DB 520 FPIFLVTLVALVDVNTGPIILAVHRTPEGVTPSMCWIRDSLVSYITNLGFSLVFLFN 579  
QY 823 VSMFIYVLVOLCRKIKKQKQAGRTSTQDLRSIAGLTFLGLITWGAFFAW--GPNVNT 880  
DB 580 MAMLATMVQILRLPHTQKWSH-----VLTLLGLSLVLGLPWLALIFSPASGTFQIV 632  
QY 881 FMYLFAINTLOGFFIFIFCYVAKENVRKQWRRLCCGKRLRAENSDWSKATNGLKQT 940  
DB 633 VLYLFIITSFQGLFIPIWY-----SMRLQARG-----GPSPLKNSD----- 671  
QY 941 VNOGVSSSSNSLQSSNSTSTTL 964  
DB 672 -----SARLPISSGSTSSRI 687

RESULT 6  
Q96HB4  
ID Q96HB4 PRELIMINARY; PRT; 693 AA.  
AC Q96HB4:  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE G PROTEIN-COUPLED RECEPTOR 56.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA, AND CHORIOCARCINOMA;  
RA Strausberg R.  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC008770; AA08770.1; -  
KW Receptor.  
SQ SEQUENCE 693 AA; 77746 MW; 5C9FA8194D1B5C50 CRC64;

Query Match 11.5%; Score 618; DB 4; Length 693;  
Best Local Similarity 28.1%; Pred. No. 4.2e-35;  
Matches 177; Conservative 114; Mismatches 245; Indels 94; Gaps 20;

QY 360 PPVKAS-----FSSPTVSAPANVNTTSA--PPVQTDIVNTSSISDLENQVLOMEKALSIG 412  
DB 133 PPLIATSVTSMWSPQNISLPSAASFTFSFSPHTAAHNASV-----DMCELKRDQL- 185  
QY 413 SLEPNLAGEMINQVSRLLHSP-----DMLAPLAQRLKLVVDIGLQLNFSNTTISTSP 467  
DB 186 -----LSQFLKHQKASRRPSAASQOQSLESKL-----TSVRFMGD 224  
QY 468 SLALAVIRVNASSNTTFFVAQDPANQVLSLETOAPENSIGTITLPSLMMNNLPAHDMEL 527  
DB 225 MVSEEDIRINATVWKLOPTAGLQDLHIHSRQEEQSEIMEYSVLLPRTLFQRTKGRGEA 284  
QY 528 ASRVQNFETPALFQDPSPLENLSLISYVSSVANLTVRNLTNRNVTTLKH-INPQDE 586  
DB 285 EKRLLLVDFSSQALFQDKNSSHV-LGEKVLGIWVQNTKVANLTPVVLTFQHQLOPK--N 341  
QY 587 LTVRCVFW-DLGRNGRGCGWDGSCVDRRLNETICTSHLTSFGVLLDLSRTSVLPQA 645  
DB 342 VTLCQVFWEDPTLSSPGHWSAGCETV--RRETQTSFCNHLTYFAVLM--VSSVEVDVAVH 399  
QY 646 MMALTFITYICGGLSSIFLSVTLVITYIAFEKTRRDYPSKILIOALCAALLNLV 699  
DB 400 KHYLSLLSYGCVVSAALACTVIAAYLCSSRPDRYTIKVMNLLAVFLDLS 459  
QY 700 FLDSWIALYKQGLCISVAVFLHYFLVFTWGLFAFMYLALVKVFNTRYIRKYILK 759  
DB 460 FLLSEPVALTGSAGCRASAIHFHLSLLTCLSMGLEGNLYRLVVEFGTVPGVYLLKL 519  
QY 760 CIVGWGPVAVVTIILTSIDPNYG--LGSYKPKPENG--SPDDFCWINNNAVFYITVVGVC 816  
DB 520 SAMGWGFPFLVTLVALVDVNTGPIILAVHRTPEGVTPSMCWIRDSLVSYITNLGLFS 579  
QY 817 VIFLLNVSMEIYVLVOLCRKIKKQKQAGRTSIQDLRSIAGLTFLGLITWGAFFAW-- 874  
DB 580 LVFLFNAMLATMVQILRLPHTQKWSH-----VLTLLGLSLVLGLPWLALIFFSAS 632  
QY 875 GPNVNTFMYLFAINTLOGFFIFIFCYVAKENVRKQWRRLCCGKRLRAENSDWSKATN 934  
DB 633 GFQLVLYLFIITSFQGLFIPIWY-----SMRLQARG-----GPSPLKNSD----- 677  
QY 935 GLKKQIVNOGVSSSSNSLQSSNSTSTTL 964  
DB 678 -----SARLPISSGSTSSRI 693

RESULT 7  
Q9Y653  
ID Q9Y653 PRELIMINARY; PRT; 693 AA.  
AC Q9Y653:  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE G-PROTEIN-COUPLED RECEPTOR.  
GN GPR56  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99168899; PubMed=10049584;  
RA Liu M., Parker R.M., Darby K., Eyre H.J., Copeland N.G., Crawford J.,  
RA Gilbert D.J., Sutherland G.R., Jenkins N.A., Herzog H.;  
RT "GPR56, a novel secretin-like human G-protein coupled receptor gene";  
RT Genomics 55:296-305(1999).  
DR EMBL; AF106858; AAD30545.1; -  
DR InterPro; IPR000873; AMP-blind.  
DR InterPro; IPR000832; GPCR\_secretin.

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DR InterPro: IPR000203; PKD_cys_rich.
DR Pfam: PF000002; 7tm_2; 1.
DR PRINTS: PF01825; GPS; 1.
DR SMART: SM00303; GPS; 1.
DR PROSITE: PS00455; AMP_BINDING; UNKNOWN.1.
DR PROSITE: PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 693 AA; 77753 MW; F7LC8E62666A5141 CRC64;

Query Match 11.5%; Score 617.5; DB 4; Length 693;
Best Local Similarity 28.3%; Pred. No. 4.6e-35;
Matches 174; Conservative 115; Mismatches 245; Indels 81; Gaps 20;

Db 360 PPVKAS-----FSSPTVSAPANVNTSA--PPVQTDIVNTSSISDLENQVLOMEKALSIG 412
Db 133 PPLATSVTSWSPONISLSAASFTSFHSPHTAAHNASV-----DMCELKRDQL- 185
QY 413 SLEPNLAGEMINQVSRLLHSP-----DMLAPLAORLLKVVDDIGLQLFNSNTTISLTP 467
Db 186 -----LSQFLKHQKASRRPSAASOOLQLESKL-----TSVRFMGD 224
QY 468 SLALAVIRVNASSNTTTFVAQDPANQVLSLETOAPENSIGITITLPSLLMNNLPAHDMEL 527
Db 225 MVSEEDRINATVWKLOQTAGLDLHIHSRQEEQSEIMEYSVLLPTLFTQTKGRSGEA 284
QY 528 ASRVQNFETPALFQDPSLENLSISYVSSVANLTVRNLTRNVTTLKH-INSQDE 586
Db 285 EKRLLLVDFSSQALFQDKNSQV-LGEKVLGVVQNTKVANLPEPVLTFFQHQLOPK--N 341
QY 587 LTRCVFV-DLGRNGRGWSDNGCSVKDRRLNETICTCSHLTSFGVLDLDSRTSVLPAQ 645
Db 342 VTLCQVFWEDPTLSSPGHWSAGCETV-RRETQSCFCNHLTYFAVLM-VSSVEVDVH 399
QY 646 MMALTFITYICGLSSIFLSVLTYYIA-----FKIRDRPSKILQICALLLNLV 699
Db 400 KHYLSLLSYGVGCVSALACLVTAAYLCRSRPLPCRRKPRDYTIKVMHNLALLAVFLDTS 459
QY 700 FLLDSWIALYKMOGLCISAVPLHFLVLSFTWGLAEFHYLALVKVFNTRYKYLKE 759
Db 460 FLLSEPVALTSEAGCRASAIPLHSLLLTCLSMWGLEGNLYRLVVEFGTYVPGYLLKL 519
QY 760 CIVGNGVPAVVVITILISPNDYG--LGSYGKPPNG-SPDDFCWINNNNAVYITVGYFC 816
Db 520 SAMGNGFFFLVTLVLDVVDVNGPILAVHRTPEGVIVPSMCWIRDSLYITNLGLFS 579
QY 817 VIFLVNSMFIVVLVOLCRKKKQKLGAKRTSIQDLRSIAGTLFLLGITWGAFFAW-- 874
Db 580 LVFLFNAMLATMVVQILRLPHTQKWSH-----VLTLLGLSLVLGLPWLALFFSFAS 632
QY 875 GPVNVTFMYLFAIFNTLQGGFFIFCYCAKENVRKQWRRYLCGKLRLAENSDWSKTATN 934
Db 633 GTFQLVLYLFLSITTSFQGLFIIFYW----SMRLQARG-----GPSPLKNSDCARL--- 681
QY 935 GLKKQTVNGQVSSSS 949
Db 682 -----PISGGTSSS 691

RESULT 8
ID Q9UHX3 PRELIMINARY; PRT; 823 AA.
AC Q9UHX3.
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE EGF-LIKE MODULE EMR2.
GN EMR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
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[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20366136; PubMed=10903844;
RA Lin H.-H., Stacey M., Hamann J., Gordon S., McKnight A.J.;
RT "Human EMR2, a novel EGF-TM7 molecule on chromosome 19p13.1, is
RL Genomics 67:188-200(2000).
DR EMBL: AF114491; AAF21974.1; -.
DR HSP; P16109; IFSB.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000832; GPCR_secretin.
DR InterPro: IPR000203; PKD_cys_rich.
DR Pfam: PF000002; 7tm_2; 1.
DR Pfam: PF000008; EGF; 2.
DR Pfam: PF01825; GPS; 1.
DR PRINTS: PR00249; GPCRSECRETIN.
DR SMART: SM00179; EGF_CA; 4.
DR SMART: SM00303; GPS; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS01187; EGF_CA; 4.
DR PROSITE: PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 823 AA; 90505 MW; ID9FA9AAA0D90553 CRC64;

Query Match 11.0%; Score 589; DB 4; Length 823;
Best Local Similarity 27.3%; Pred. No. 5.9e-33;
Matches 247; Conservative 120; Mismatches 327; Indels 212; Gaps 46;

QY 158 PQNHITNGTL-----TGVLSLSLSEKRS-----ELNK--TLQILSETYFIMCATAEAGST 205
Db 34 PODSSCVNATACRCNPGFSFSEIITTPMETCDDINECATILSKVSCGKFSDCWTEGYSYD 93
QY 206 LNCI-----FTIKLNTNMNACAII-----AALERVK 231
Db 94 CVCSPGYEVPVSGAKTFK-NESENTQDQVDECCQNPRLCKSYGTCVNLGSGTCQCLPGFK 152
QY 232 IRPME-----HCCSVRIPCSPSP---BELGKLOCDLQDPIVCLADHPHPPFPSSQS 281
Db 153 LKPEDPKLCTDYNECTSGQNPCHSSTHCLNNVSGYOCRCR-----PGWQPIPGS-- 201
QY 282 IPVPRATVLSQVPKATSAEPDPYSPVTHN-VPSPTGEIQP-LSPQPSAPIASSPAIDM 339
Db 202 -PNGPNNTVCEDVDECSGGHQCDSDSTVCFNTVGSYSCRCRPGMKPRHGIP----- 251
QY 340 PQSETISSPMPTQVHSGTTPPVKASFSPTVSAPANVNTTSAPPVQTDIVNTSSISDLE 399
Db 252 NNQKDTVCEDM--TFSTWTPPP-----GVH 274
QY 400 NOVLO--MEKALSLG-SLEPNLAGEMINQV-----SRLHSPDM-LAP-----LAQRLL 445
Db 275 SQTLSRFFDKVQDLGRDYKPLANNTIQSILQALDELLEAPGDLTLPRLQOHCVASHL 334
QY 446 KVDDI--GLQNFNTTISLTSPS---LALAVTRVNASSSENTTTFVAQDPANQVLSLET 500
Db 335 DGLVDVLRGLSKNLSNGLNFSYPAGTELSLEV---QKQVDRSVTLRQNAVMQMDW-N 389
QY 501 QAPENS-----IGTITLPSLLMNNLPAH-DMELASRVQENFFET-PALFQDPSLENLSL 552
Db 390 QAKSGDGPSPVGLVSIIPG--MGKLLAEAPLVLEPEKQMLLHETHOGLLODGS---PIL 444
QY 553 ISYVISSVANLTVRNLTRNVTTLKH--INPSODELTVRVFWDLGNRGGRGGSDNCC 610
Db 445 LSDVISAFLSNNDTNLSSPVTFTHSRSVTPRQ---KVLGVFWHGQN-GCGHWATTGC 500
QY 611 SVKDRRLNETICTCSHLTSFGVLL---DLSTSVLPQAQMALTFTTYICGGLSSIFLSVT 667
Db 501 STTGTRDTSTICRCHTLSSFAVLMAHYDQVEDPV-----LTVITYMGLSVSLCLLIA 554
QY 668 LVTYIAFEKIRDRDVPKSKILQICALLLNVLFLDLSWIALYKMOGLCITSVAVFLHYFL 727
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Db 555 ALTFLLCKAIONTS-TS-LHLQLSLCLFLAHLFLVAIDQTGHKV--LCSIIAGTLHYLYL 611
Qy 728 VSTWMLGLEAFHMYLA--LVKVFENTYRKYLKFCI-VGWGVPVAVVVIILITSPDNYG 783
Db 612 AFTTWMLLEALYLFELARNLTVVNYSINRPMKLMFPVGVGPVAVTVAISARPHLYG 671
Qy 784 LGSYGKFPNGSPDFCWINNNAVFIITVVGFCVIFLLNVSMFIVVL-VOLCRKIKK-KKQ 841
Db 672 TFSR-----CWLOPEKGFIMGLFGPVCAIFSNNLVFLVTLWTLKKNRLLSSNSE 720
Qy 842 LGAQRKTSIOLRSIAGLTLLGLTGWCFARFANGPVNVTFMYLFAIFNVLQGFIFIFYC 901
Db 721 VSTLRNTRMLAKTAQL-FILGTCWGLQLOVGAARVMAYLFTIINSLOQGVIFPLVYC 779
Qy 902 VAKENVKQRRYLCGCKLRLAENSDKSTATNGLKQTVNQGVSSNSLQSSNSTNS 961
Db 780 LLSQVQREY-----GK-----WSK-----GIRKLK-----TESEMHILSSAKADYS 817
Qy 962 TLLIYN 967
Db 818 KPSTVN 823

RESULT 9
ID 095490 PRELIMINARY; PRT; 1403 AA.
AC 095490;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-OCN-2001 (TREMBLrel. 18, Last annotation update)
DE LATROPHILIN-2.
GN LPHL OR LECI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1.
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Isolation and characterization of a human homologue of the
RT latrophilin gene from a region of lp31.1 implicated in breast
RT cancer.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN 2.
RP SEQUENCE FROM N.A.
RA MEDLINE=99153747; PubMed=10030676;
RX White G.R.M., Varley J.M., Heighway J.;
RT "Isolation and characterisation of a human homologue of the
RT latrophilin gene from a region of lp31.1 implicated in breast
RT cancer.";
RL Oncogene 17:3513-3519(1998).
RN 3.
RP SEQUENCE FROM N.A.
RA White G.R.M., Varley J.M., Heighway J.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN 4.
RP SEQUENCE FROM N.A.
RA Hayflick J.S.;
RT "Lectomedin-1 gamma.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN 5.
DB EMBL; AJ131581; CAA10458.1;
DB EMBL; AJ244492; CAB60229.1;
DB EMBL; AJ244493; CAB60229.1; JOINED.
DB EMBL; AJ244494; CAB60229.1; JOINED.
DB EMBL; AJ244496; CAB60229.1; JOINED.
DB EMBL; AJ244497; CAB60229.1; JOINED.
DB EMBL; AJ244498; CAB60229.1; JOINED.
DB EMBL; AJ244499; CAB60229.1; JOINED.
DB EMBL; AJ24501; CAB60229.1; JOINED.
DB EMBL; AJ244502; CAB60229.1; JOINED.
DB EMBL; AJ244503; CAB60229.1; JOINED.
DB EMBL; AJ244504; CAB60229.1; JOINED.

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DR EMBL; AJ244505; CAB60229.1; JOINED.
DR EMBL; AJ244506; CAB60229.1; JOINED.
DR EMBL; AJ244507; CAB60229.1; JOINED.
DR EMBL; AJ244510; CAB60229.1; JOINED.
DR EMBL; AJ244511; CAB60229.1; JOINED.
DR EMBL; AJ244512; CAB60229.1; JOINED.
DR EMBL; AJ244516; CAB60229.1; JOINED.
DR EMBL; AF104939; AAD54677.1;
DR InterPro; IPR000922; Gal_lectin.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR003334; Latrophilin.
DR InterPro; IPR003112; Olfac_like.
DR InterPro; IPR000203; PKD_cys_rich.
DR InterPro; IPR002088; PPTA.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02140; Gal_Lectin; 1.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR Pfam; PF02354; Latrophilin; 1.
DR Pfam; PF02191; OLF; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR ProDom; PD005612; Gal_lectin; 1.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; HormR; 1.
DR SMART; SM00284; OLF; 1.
DR PROSITE; PS50227; G-PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G-PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS00904; PPTA; UNKNOWN_1.
DR PROSITE; PS50228; SUBLECTIN; 1.
DR SEQUENCE 1403 AA; 157176 MW; CE43AB82916D0D35 CRC64;

Query Match 10.1%; Score 539; DB 4; Length 1403;
Best Local Similarity 26.6%; Pred. No. 4e-29;
Matches 213; Conservative 120; Mismatches 333; Indels 134; Gaps 34;

Qy 286 PRATVLSQVPKATFAEPDYPVTHNVPSPIGEIQPLSPQSPAPIASSPAIDMP--PQS 343
Db 429 PMSTVAGSQEGSKGTKPP-AVSTTKIP-PITNIFPL-PERFCEALDSKGKWPOTQRG 485
Qy 344 ETISPMQTHVSGTPPVKASFSSPTVSAPANVTTSAPPVQTDIVNTSS--ISDLENO 401
Db 486 MVVERPCPK---GT-----RGTASYLCMLSTGTWNPKGPDLSNCTSHWNQLAQK 532
Qy 402 VLQMEKALSLG-----SLEPNLAGEMINOVSRLLHSPDML-APLAQRLLKVDDIGLQ 454
Db 533 IRSGENAASLANELAKHTKGPVFGDVSSV-RLMEOLVDILDALQELKPEKSDSAGRS 591
Qy 455 LN--FSNTTISUTSPSLAVIRVNAS-SFNNTT-----FVAQDPANL-----QVS 497
Db 592 YNKATVDTVDNLLRPEALESWKHNSSEQAHTATMLDTEEGAFVLAD--NLLEPTRVS 649
Qy 498 LETO-----APENSIGTTITLPSLMN-----NLPAHDMELASR---VQFNFFETPA 540
Db 650 MPTENIVLEAVLSTEGQIQDFKFKPLGKAGAGSIQISANTVKONSRLAKLFIYRS 709
Qy 541 LFODPSLEN-----LSLISYVIVSSSVANLTVR-NLTNRVTVTLKHINPSQ 584
Db 710 LGQFLSTENATIKLGADFIGRNSTIATVNSHVISVSNKESRVLTPDVLTPHIDP-D 768
Qy 585 DELTVRCVFWDLGRNGRGSGSDNGCSVKDRRLNETICTCSHLTSGVLLDLSRTSVLP- 643
Db 769 NYFNANCSFWNYSERTMMGYSTQCKLVDTNKTTRTCACSHLTNFAILLMAHRIAYKDG 828
Qy 644 AQMWALFYIYGGLSSIFLTVTYIAFEKIRKRDYPSKILIQCAALLLVLLD 703
Db 829 VHELLLTVTITWVGIVISLVCLAICITFCFRGLQSD-RNTIHKNLICINLFAIEFILI 887
Qy 704 SWIATYKMQGLCISVAVFLHYFLVSVTWMGLEAFHMYLALVKVFT-YIRKYILLKFCIV 762
Db 888 --IDTKYATACPIFAGLLHFFFLAAFWMCLEGVOLYMLVEVFSEYSRKKY--YVVA 943

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QY 763 GNGVPAVVTIITLSPDNTGLSGYKFPNGSPDDFCWNNNAVYITVVGVCVIFLLN 822  
DB 944 GYLFPATVVGSAIDYKSYG-----TEKACWLVHDVNFYFWSFIGFVTFIILLN 992  
QY 823 VSMFIVVLQCLRIKKKQOLGAOKTTSIQDLRS-IAG-----LTFLLGITWGAFFAWGPVN 878  
DB 993 I---IFLVITLCRWKHSNLTLPDSSSLENIKSWVLGAFALLCLLGLTWSGULLFINEET 1049  
QY 879 VTPMYLFAINTLQGGFFIFCYCAKENVRKQW-----RRYLCCGKL----- 920  
DB 1050 IVMAYLFTIENAGQGVFIFFHFCALQKKVRKEYGKCFRHSYCCGGLPTESPSSVKASTP 1109  
QY 921 -RLAENSNDWKATNGLKQKTVNGVGVSSSSSLOSSNSTSTTLLVNDCSVHAGS--- 976  
DB 1110 RTSARYSSGTSQSRIRRMWMDTVRKQSESSFGDINSTLNGHSLNARDTSAMDITLP 1169  
QY 977 -NGNASTERNGVSFSVQNGD 995  
DB 1170 LNCNFNN-----SVSLHKGD 1184  
RESULT 10  
O97823 PRELIMINARY; PRT; 1283 AA.  
AC O97823  
DT 01-MAY-1999 (TREMREL. 10, Created)  
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)  
DT 01-OCT-2001 (TREMREL. 18, Last annotation update)  
DE LATROPHILIN 3 SPLICE VARIANT ABBH.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99148828; PubMed=10025961;  
RA Matsushita H., Lellanova V.G., Ushkaryov Y.A.;  
RT "The latrophilin family: multiply spliced G protein-coupled receptors  
with differential tissue distribution.";  
RL EMBL Lett. 443:348-352(1999).  
DR EMBL; AF11090; AA05326.1; .  
DR InterPro; IPR000922; Gal\_Lectin.  
DR InterPro; IPR000832; GPCR\_secretin.  
DR InterPro; IPR001879; hormo\_receptor.  
DR InterPro; IPR003334; Latrophilin.  
DR InterPro; IPR003112; Olfac\_like.  
DR InterPro; IPR000203; PKD\_cys\_rich.  
DR Pfam; PF00002; 7tm\_2; 1.  
DR Pfam; PF02140; Gal\_Lectin; 1.  
DR Pfam; PF01825; GPS; 1.  
DR Pfam; PF02793; HRM; 1.  
DR Pfam; PF02354; Latrophilin; 1.  
DR Pfam; PF02191; OLF; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PRODOM; PD005612; Gal\_Lectin; 1.  
DR SMART; SM00303; GPS; 1.  
DR SMART; SM00008; Hormr; 1.  
DR SMART; SM00284; OLF; 1.  
DR PROSITE; PS50227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
DR PROSITE; PS50261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
DR PROSITE; PS50228; SUEL\_LECTIN; 1.  
SQ SEQUENCE 1283 AA; 143897 MW; 9D87F15DD6001EC0 CRC64;

Query Match 10.0%; Score 536.5; DB 6; Length 1283;  
Best Local Similarity 23.7%; Pred. No. 5.3e-29;  
Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;  
QY 260 LQDPTVCLADHPGPPFSSSQSIPVVRATVLSQVPKATSFAPPDYSPVTHNVFSPIGE 319  
DB 409 ISPPHLSDLERPPVREISTTGTGLTGTSTTTTLRTTT-----WSPGRKSTTPSVSGR 462

QY 320 IQPLSPOPSAPIASSPAIDMPPQSETISSPMPQTHVSTPPPVKASFSS----- 368  
DB 463 RNKSTSTP-----SPAELVNDI-----TTHVPSASPOIPALEESCEAVEAREIMW 508  
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVLOMEKALS 410  
DB 509 FKTRQOGMAKQPCPAGTIGVSTYLCAPDGIWDGPGDLSNCS--SPWVNHITQKLRS-- 564  
QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440  
DB 565 -GETAANIARELAETRNHLNAGDITYSVRANDQLVGLLDVQLRNLTPGKDSAAARSLNK 623  
QY 441 -----AQRLLKYVDDIGLQNFN-----TTISLSPSLALAVIR-----VNAS 479  
DB 624 LQKRSCRAYVQAMVETVNNL-LQPQALNAWRDLTTSQDLRAATMLDITVEESAFVLAD 682  
QY 480 SFNTTTFVAQDPANLOVSELTQAPENSIGTITLPSSL-----MNNLPAMDLMELASR 530  
DB 683 NLLKTDIVRENTDNTQLEVARLSTEGNLEDLKFPENTGHGTTIQLSANTLUKQNGRGEIR 742  
QY 531 VOENFFET--PALFODPSLENLSL-----ISYVISSSVANLTVRN-----LTR 571  
DB 743 VAFVLYNNLGPYL-----STENASMKLGTAMSTNHSVIVNSPVITAAINKEFSNKVYLAD 798  
QY 572 NVTYTLKHINPSQDELTVRVCFWDLGRNGRGWSDNGSCVKDRRLNETICTCSHLTSFG 631  
DB 799 PVFETVHKIKQSEENFNPCSFWSYKRTMTGYWSTQGGRLTLTKNTHHTTCSNHLTNFA 858  
QY 632 VLL---DLSRTSVLPAQMMALFIYIGGLSIFSLVTLVTYIAFEKIRRDYPSKILIQ 688  
DB 859 VLMARVVKHSDAV--HDLDDVITWVGILLSLVCLLICIFTCFFRGLQSD-RNTIHN 915  
QY 689 LCAALLNLNLVFL-----DSWIALYKMOGLCISAVFVLFVLLVSTWGLFAFHMYLA 743  
DB 916 LCISLFAVELLFLIGINTDQPIA-----CAVFAALLHFFFLAFTWMELEGVQLYIM 968  
QY 744 LVKVENT--YIRKYILKFCIVGWGPVAVVTIILTSPDNVGLSGYCKFPNGSPDDFCWI 801  
DB 969 LVEFPESEHSRKY---FYLVGMPALIVAVSAADYRSYG-----TDKVCWL 1014  
QY 802 NNAVYITVVGVCVIFLLNVSMFIVLVVLQLCRIKK--KKQLGAQRKTSIQDLR----- 854  
DB 1015 RLDYTFIWSFIGPATLIIMLVIFGLIYALYKMFHTAILKPESCLDNINYEDNRPFKS 1074  
QY 855 ---STAGTFLLGITWGAFFAWGPVNVTVMYLPALTNTLOGFFIFCYCAKENVRKQW 911  
DB 1075 WVIGAIALLCLLGLTWAFLMYINESTVIMAYLFTIFNSLQGMFIFIFHCVLQKKVRKEY 1134  
QY 912 RRYL--CC-----GKRLAENSNDWKATNGLKQKTVNGVGVSS 948  
DB 1135 GKCLRTHCCSGRSTESSIGSGKTSRTPGYSTGSRIRRMWMDTVRKQSESSFITGD 1194  
QY 949 SNSLOSSNSTSTTLLVNDCSVHAGSN 977  
DB 1195 INSSASLNRGAMANHLISNALLRPHGTNN 1223  
RESULT 11  
O97829 PRELIMINARY; PRT; 1351 AA.  
AC O97829  
DT 01-MAY-1999 (TREMREL. 10, Created)  
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE LATROPHILIN 3 SPLICE VARIANT BBHH.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99148828; PubMed=10025961;

RA Matsushita H., Lelianova V.G., Ushkaryov Y.A.;  
 RT "The latrophilin family: multiply spliced G protein-coupled receptors  
 RL FEBS Lett. 443:348-352(1999).  
 DR EMBL: AF111096; RAD05332.1;  
 DR InterPro: IPR000922; Gal\_lectin.  
 DR InterPro: IPR000832; GPCR\_secretin.  
 DR InterPro: IPR001879; hormn\_receptor.  
 DR InterPro: IPR003334; Latrophilin.  
 DR InterPro: IPR003112; Olfac\_like.  
 DR InterPro: IPR000203; PKD\_cys\_rich.  
 DR Pfam: PF00002; 7tm\_2; 1.  
 DR Pfam: PF02140; Gal\_lectin; 1.  
 DR Pfam: PF01825; GPS; 1.  
 DR Pfam: PF02793; HRM; 1.  
 DR Pfam: PF02354; Latrophilin; 1.  
 DR Pfam: PF02191; OLF; 1.  
 DR PRINTS: PR00249; GPCRSECRETIN.  
 DR PRODOM: PD005612; Gal\_lectin; 1.  
 DR SMART: SM00303; GPS; 1.  
 DR SMART: SM00008; Hormr; 1.  
 DR SMART: SM00284; OLF; 1.  
 DR PROSITE: PS50227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE: PS50261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 DR PROSITE: PS50228; SUEL\_LECTIN; 1.  
 DR SEQUENCE 1351 AA; 150807 MW; 7C085DE9224C742A CRC64;

Query Match 10.0%; Score 536.5; DB 6; Length 1351;  
 Best Local Similarity 23.7%; Pred. No. 5.7e-29;  
 Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;

QY 260 LQDPIVCLADHPRGPFSSQSIPVVPVATVLSQVPKATSAEPDPYSPVTHNVPSPIGE 319  
 DB 477 ISPPHLDSDLERPPVREISTTGLTGTSTTTTLRTTT-----WSPGRSTTPSVSCR 530

QY 320 IQPLSPQPSAPIASSPAIDMPPQSETISSPMQTHVGTCTPPVVKASFSS----- 368  
 DB 531 RNRSTSTP-----SPAIEVLNDI-----THVPSASQIIPALESCAEAREINMW 576

QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVLMKEALS 410  
 DB 577 FKTRQGMKQPCPACTGIVSTYLCIAPDGIWDPGQDLSNCS--SPWNHITQKLKS-- 632

QY 411 LGSLEPNLAGEMINQSVRLHS-----PPQMLAPL----- 440  
 DB 633 -GETAANTARELAETRNHNLNAGDIYSVRAMDQVLGLLDVQLRLNLTPEGKDSAARSLNK 691

QY 441 -----AQLKLVDDIGLQLNFSN-----TTISLTSPSLALAVIR-----VNAS 479  
 DB 692 LQKRERSRAYVQAMVETVNNL-LQPOLNARDLTTSQDLRAATMLLDVVEESAFVLAD 750

QY 480 SFNTTTFVAQDPANLOVLSLETQAPENSIGTITLPSSL-----MNNLPAHDMELASR 530  
 DB 751 NLLKTDIVRENDIIOLEVARISTECNLEDLKPFGTNGHSTIQLSANTLKQNGRNGEIR 810

QY 531 VQNFET--PALFODPSLENLSL-----ISYVISSVANLATVRN-----LTR 571  
 DB 811 VAFVLYNNGPYL-----STENASMKLGTEAMSNHSIVNSPVITAINKEFSKNVYLAD 866

QY 572 NVTYTLKHINFSQDELTVRCVFDWLGNGRGWSGNGSCVKORRLNETICTCSHLTSFG 631  
 DB 867 PVVFTVKHIKQSEENFNCFSEWSYSKRTWGTGYSQGCRLTLTKTKTSCNHLTNFA 926

QY 632 VLL---DLRSVSLPAQMAALFFIYIGGLSIFLSVTLVTVYIAFEKIRRDYFSKILIQ 688  
 DB 927 VLMHVEVKHSDAV--HDLLEDVITWIGILLSVLVCLICIFTECFRGLQSD-RNTIHN 983

QY 689 LCAALLNLNLFLL-----DSWIALYKMOGLCISAVFLHYFLLVSTFTWMLGFHMYLA 743  
 DB 984 LCISLFAELFLIGINTDQPIA-----CAVFAALLHFFFLAATWFLFEGVQLIYM 1036

QY 744 LVKFVNT--YTRKYLKFCIVGWGVPVAVVITILITSPDNYGLGSYGKFPNGSPDDFCWI 801

Db 1037 LVEVFESEHSRRKY---FYLVGYGMPALIVAVSAADYRSYG-----TDKVCWL 1082  
 QY 802 NNAVFYITVGVFCVIFLLNVSMFIVVLVOLCRIKK--KKOLGAQRKKTSTODLR----- 854  
 Db 1083 RLDTYFTWFSFGPATLIIMLVNFIAGIALYKMFHTAILKPESGCLDNIYEDNRPFIKS 1142  
 QY 855 ---SIAGLTGELLGTWGFAPFAFWGVNVTMYLFAIFNTLQGFIFIFCYCAKENVRKQW 911  
 Db 1143 WVIGATALLCLGLTWAFGLMYNESTVIMAYLFTIFNSLQGMFIEIFHCVLQKKVKEY 1202  
 QY 912 RRYL---CC-----GKLRLENSDWSKTATNGLKKQTWVNGVSSS 948  
 Db 1203 GKCLRHCCSGRSTESSIGSOKTSGSRTPGRYSTGQSQRIRRMWNTVVRKQSESSFITGD 1262  
 QY 949 SNSLQSSNSTNTLLVNNDCSVHASGN 977  
 Db 1263 INSSASINRGAMANHLISNALLRPHGTNN-1291

## RESULT 12

Q97821 PRELIMINARY; PRT; 1512 AA.  
 ID O97821  
 AC O97821;  
 DT 01-MAY-1999 (TReMBLrel. 10, Created)  
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)  
 DE LATROPHILIN 3 SPLICE VARIANT ABBF.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_taxid=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-99148928; PubMed-10025961;  
 RA Matsushita H., Lelianova V.G., Ushkaryov Y.A.;  
 RT "The latrophilin family: multiply spliced G protein-coupled receptors  
 RT with differential tissue distribution."  
 RL FEBS Lett. 443:348-352(1999).  
 DR EMBL: AF111088; RAD05324.1; --  
 DR InterPro: IPR000922; Gal\_lectin.  
 DR InterPro: IPR000832; GPCR\_secretin.  
 DR InterPro: IPR001879; hormn\_receptor.  
 DR InterPro: IPR003334; Latrophilin.  
 DR InterPro: IPR003112; Olfac\_like.  
 DR InterPro: IPR000203; PKD\_cys\_rich.  
 DR Pfam: PF00002; 7tm\_2; 1.  
 DR Pfam: PF02140; Gal\_lectin; 1.  
 DR Pfam: PF01825; GPS; 1.  
 DR Pfam: PF02793; HRM; 1.  
 DR Pfam: PF02354; Latrophilin; 1.  
 DR Pfam: PF02191; OLF; 1.  
 DR PRINTS: PR00249; GPCRSECRETIN.  
 DR PRODOM: PD005612; Gal\_lectin; 1.  
 DR SMART: SM00303; GPS; 1.  
 DR SMART: SM00008; Hormr; 1.  
 DR SMART: SM00284; OLF; 1.  
 DR PROSITE: PS50227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE: PS50261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 DR PROSITE: PS50228; SUEL\_LECTIN; 1.  
 DR SEQUENCE 1512 AA; 169140 MW; 792CDD8790C4AA9B CRC64;

Query Match 10.0%; Score 536.5; DB 6; Length 1512;  
 Best Local Similarity 23.7%; Pred. No. 6.6e-29;  
 Matches 206; Conservative 124; Mismatches 334; Indels 205; Gaps 30;

QY 260 LQDPIVCLADHPRGPFSSQSIPVVPVATVLSQVPKATSAEPDPYSPVTHNVPSPIGE 319  
 Db 409 ISPPHLDSDLERPPVREISTTGLTGTSTTTTLRTTT-----WSPGRSTTPSVSGR 462

QY 320 IQPLSPQPSAPIASSPAIDMPPQSETISSPMQTHVGTCTPPVVKASFSS----- 368



Db 1037 LVEVFESEHRRKY---FYLVGVGMPALIVAVSAADYRSYG-----TDKVCWL 1082  
 Qy 802 NNAVFYITVGVYFCVIFLNVSMFIVVLVOLCRKIK--KKOLGAQRKTSIODLR-----854  
 Db 1083 RLDYFIWFGIPATLIIMLVFLGIALYKMFHTTALKPESGCLDNIYVENDRPFIFKS 1142  
 Qy 855 ---STAGLFLGLITWGFAPFANGPVNVTFMYLFAIPNTLQGGFFIFCYCAKENVRKOW 911  
 Db 1143 WYVIGAIALLCLLGLTWAFGLMYINESTVIMAYLTFITNSLQGMFFIEHCVLQKKVKEY 1202  
 Qy 912 RYL---CC-----GKRLAENSDDSKTATNGLKQTVNQGVSS 948  
 Db 1203 GKCLRTHCGSGRSTESSIGSGKTSGSTPTGRYSTGSGSRIIRMMNDTVRKQSESSFITGD 1262  
 Qy 949 SNSLQSSNSTNTSTLLVNNDCSVHASGN 977  
 Db 1263 INSSASLNKGAMANHLSNALLRPHGTNN 1291

RESULT 14  
 O88927 PRELIMINARY; PRT: 1527 AA.  
 AC O88927; O88924; O88928; O88929; O88926; O88925;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE CALCIIUM-INDEPENDENT ALPHA-LATROTOXIN RECEPTOR 3 PRECURSOR (LATROPHILIN  
 DE 3) (LRP3) (CIRL) (CL3) (LPH3).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP MEDLINE=99047651; PubMed=9830014;  
 RX Sugita S., Ichtchenko K., Khivotchev M., Suedhof T.C.:  
 RA "alpha-latrotoxin receptor CIRL/latrophilin 1 (CL1) defines an unusual  
 RT family of ubiquitous G-protein-linked receptors. G-protein coupling  
 RT not required for triggering exocytosis.";  
 RL J. Biol. Chem. 273:32715-32724(1998).  
 CC -!- FUNCTION: PERFORMS A GENERAL AND UBIQUITOUS FUNCTION AS G-PROTEIN-  
 CC COUPLED RECEPTORS IN CELLULAR SIGNALING.  
 CC -!- SUBUNIT: HETERODIMER OF A 120 AND A 85 KDA SUBUNITS THAT ARE THE  
 CC RESULT OF ENDOGENOUS PROTEOLYTIC CLEAVAGE OF THE PRECURSOR.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- ALTERNATIVE PRODUCTS: SIX ISOFORMS; CL3AA, CL3AB, CL3AC, CL3BB,  
 CC CL3BC, AND CL3BA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -!- TISSUE SPECIFICITY: BRAIN.  
 CC -!- PTM: CLEAVED INTO A 120 KDA HYDROPHILIC GLYCOSYLATED EXTRACELLULAR  
 CC SUBUNIT WHICH CONTAINS AT LEAST PART OF ALPHA-LATROTOXIN-BINDING  
 CC SITE, AND A 85 KDA MEMBRANE-SPANNING SUBUNIT THAT REMAIN STILL  
 CC TIGHTLY BOUND TO EACH OTHER AFTER PROTEOLYTIC CLEAVAGE (BY  
 CC SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -!- SIMILARITY: SOME, TO NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED  
 CC PROTEINS.  
 CC EMBL; AF081157; AAC62663.1; -;  
 CC EMBL; AF081154; AAC62660.1; -;  
 CC EMBL; AF081158; AAC62664.1; -;  
 CC EMBL; AF081159; AAC62665.1; -;  
 CC EMBL; AF081156; AAC62662.1; -;  
 CC EMBL; AF081155; AAC62661.1; -;  
 CC InterPro; IPR000922; Gal\_lectin.  
 CC InterPro; IPR000832; GPCR\_secretin.  
 CC InterPro; IPR001879; hormn\_receptor.  
 CC InterPro; IPR003334; Latrophilin.  
 CC InterPro; IPR003112; Olfac\_like.  
 CC InterPro; IPR000203; PKD\_cys\_rich.  
 CC Pfam; PF000002; 7tm2; 1.  
 CC Pfam; PF02140; Gal\_Lectin; 1.  
 CC Pfam; PF01825; GPS; 1.  
 CC Pfam; PF02793; HRM; 1.

pfam; PF02354; Latrophilin; 1.  
 pfam; PF02191; OLF; 1.  
 ProDom; PD005612; Gal\_lectin; 1.  
 SMART; SM00303; GPS; 1.  
 SMART; SM00008; Hormr; 1.  
 SMART; SM00284; OLF; 1.  
 PROSITE; PS0227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 PROSITE; PS0261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 PROSITE; PS0228; SUEL\_LECTIN; 1.  
 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 ?  
 FT CHAIN 1 ?  
 FT RECEPTOR 3  
 FT CALCIIUM-INDEPENDENT ALPHA-LATROTOXIN  
 FT EXTRACELLULAR (POTENTIAL).  
 FT CYS-RICH, LECTIN-LIKE.  
 FT OLFACTOMEDIN-LIKE.  
 FT PRO-RICH.  
 FT SER/THR-RICH.  
 FT BAI.  
 FT CYS-RICH.  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT POTENTIAL.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT POTENTIAL.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT POTENTIAL.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT POLY-ALA.  
 FT CLEAVAGE (POTENTIAL).  
 FT MISSING (IN CL3AA, CL3AB, AND CL3AC).  
 FT GLNNARDTSVMDTFLPNGHNSYSIAGVEYLSNC -> P  
 FT YRETSMGVKNIAVQIGASECGQKCHGYSTEW (IN  
 FT CL3BB AND CL3AB).  
 FT MISSING (IN CL3BB AND CL3AB).  
 FT EGLNNARDTSVMDTFLPNGHNSYSIAGVEYLSNCVQII  
 FT DRGYNHNETALEKKILKELTSNYIPSYLNHRSSEQR  
 FT -> GTMAHLMSNALLRPHGTNNPVTLLGEPAVCNPSIS  
 FT MYNAQEPYRSTSCVKNIAVQIGASECGQKCHGYSTTE  
 FT W (IN CL3AC AND CL3BC).  
 FT MISSING (IN CL3AC AND CL3BC).  
 FT VARSPLIC 1342 1527  
 FT VARSPLIC 1527 AA; 169779 MW; A0F1FEC2D9B50B9F CRC64;  
 SQ

Query Match 10.0%; Score 536; DB 11; Length 1527;  
 Best Local Similarity 24.7%; Pred. No. 7.3e-29;  
 Matches 218; Conservative 131; Mismatches 344; Indels 190; Gaps 35;

Qy 248 SSPEELGLQCDLPVCLADHPGPPFSSSSQIPVVRATVLSQVPKATSFAPPDYS 307  
 Db 466 GGPVHHGVSY-ISPIHLDSLERPVRGISTGPGMGSTTTTTLRTTWNLRSTT 524  
 Qy 308 PV-----THNVSPGIGIQLSPQSPAPIASPAIDMPQSETISSPMPQTHVSGTPP 360  
 Db 525 PSLFGRNRSTSTSPS--AIEVLDDVTTHLPSSAASQIPAMESCEAVEAREIMWFKTRQG 582  
 Qy 361 PVKASFSPTVS-----APANVNTSAPPQTDIVNTSSISDLENQVLOMEKALSLS 413  
 Db 583 VAKOSCPAGTIGVSTVYLCIAPDGIWDPQG-----DUSNCS--SPWVNHIQKLKS---GE 633  
 Qy 414 LEPNLAGEMINQVSRLLHS-----PPDMLAPL-----440  
 Db 634 TAANIARELAETRNHLNAGDITYSVRAMDQVLGLLDVQLNLTGPKGDSARSINKLQK 693  
 Qy 441 -----AQRLLKVVDDIGLQNFN-----TTISLTSPSLALAVIR-----VNASSFN 482

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Db 694 RERSCRAYQAVMETVNNL-LQPQALNAWRDLTTSQDLRAATMLLDTVEESAFVLADNLL 752
QY 483 TTTTFVAQDPANLQVSLQTPENSIGTITLPSSL-----MNNLPAHDMELASRVQF 533
Db 753 KTDIVRENTDNIQLEVARLSTEGNLEDKPEPTGHTGHTSTIOLSAANTLKQNGRNGEIRVAF 812
QY 534 NFET--PALFQDPSPLENLSL-----ISVVISSVANLTVRN-----LTVNVT 574
Db 813 VLYNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAAINKFESKVKYVLADPV 868
QY 575 VTIKHNPSQDELTVRCVFDLGRNGRGWSDNGSCSVKDRRLNETICTCSHLTSGVLL 634
Db 869 FIVKHIKQSEENFNCSEFWSYKRTWTGWSGTQGRLLTNTKTHHTTCSNHLTNFAVLM 928
QY 635 ---DLRSTSVLPQAMALFTIYIGGLSSIFSLVTLVITYIAFEKIRDYPSKILLIQLCA 691
Db 929 AHVEVHKSDAV--HDLDDVITWVIGILLSVCLLCITFTCFRGLQSD-RNTIHKNL 985
QY 692 ALILLNLVFL-----DSWIALYKMGGLCISVAVFLHYFLVSVTWMLGFAFMYLALVK 746
Db 986 SLFVAELLFLIGINRTOPTA-----CAVFAALLHFFFLAAFTWMLFEGVQLYIMLVE 1038
QY 747 VENT--YIRKYILKFCIVGVAVVTVITLTISPDNVLGSGYKFPNGSPDDFCWNN 804
Db 1039 VFSEHSRRKY---FVLVGYGMPALIVAVSAVDYRSYG-----TDKVCWLRD 1084
QY 805 AFVYITVGVFCVIFLLNVSMFIVLVQLCRIKK--KKOLGAQRKTSIODLRSIAGLTFL 862
Db 1085 TYFIWFGPATLIIMLVIFLGLYALYKMFHTTALPKESGLDNKISWVIGAI-LCL 1143
QY 863 LGITWGAFFAFGPNVNTFMFLAINTLQGGFIIFYCVAKENVRKQW---RRYLCCG 918
Db 1144 LGITWAGLWYNINVESTIMAYLFTIENSLOGMFIPIHCVLQKVKYKGLRTHCCSG 1203
QY 919 KL-----RLAEND-----WSKATNGLKKQTVNGVSSSSNSLQSS 955
Db 1204 KSPSSIGSGKTSGRTPGYSQSRIRRMWNT-----VRKOSSEFITGDIN-----S 1255
QY 956 SNTNSTTLLVN--NDCSVHAS--GNGNASTERNRGVSFVQNGD 995
Db 1256 SASLREGLNARDTSVMDTLPNGN-----HGNSYSIAGGE 1293
Db
RESULT 15
O97820 PRELIMINARY; PRT; 1274 AA.
AC O97820;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE LATROPHILIN 3 SPLICED VARIANT ABAB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148828; PubMed=10025961;
RA Matsushita H., Lelianaova V.G., Ushkaryov Y.A.;
RT "The latrophilin family: multiply spliced G protein-coupled receptors
RL with differential tissue distribution.";
RL FEBS Lett. 443:348-352(1999).
DR EMBL; AF111087; AAD05323.1;
DR InterPro; IPR000922; Gal.lectin.
DR InterPro; IPR000832; GPCR-secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR003334; latrophilin.
DR InterPro; IPR003112; Olfac_like.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02140; Gal.lectin; 1.
DR Pfam; PF01825; GPS; 1.
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DR Pfam; PF02793; HRM; 1.
DR Pfam; PF02354; Latrophilin; 1.
DR Pfam; PF02191; OLF; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRODOM; PD005612; Gal_lectin; 1.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; Hofmr; 1.
DR SMART; SM00284; OLF; 1.
DR PROSITE; PS02027; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02061; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS02228; SUEL_LECTIN; 1.
SQ SEQUENCE 1274 AA; 142748 MW; 147C1B5FC160037F CRC64;

Query Match 10.0%; Score 534; DB 6; Length 1274;
Best Local Similarity 23.9%; Pred. No. 7, 9e-29;
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;

QY 260 LQDPVCLADHPGPPFSSQSIPIVPRATVLSQVPKATSFABPPDYSPTVTHNVPSPIGE 319
Db 409 ISPPHLDSDLERPPVREISTTGLTGTSTTTLRTTT-----WSPGRSTTPSVSGR 462
QY 320 IQPLSPOPSAPIASSPALDMPQSETISSPMPOTHVSGTPPVKASFSS----- 368
Db 463 RNRSTSTP-----SPALEVLNDI-----TTHVPSASPOIPALEESCEAVEAREIMW 508
QY 369 -----PTVSAPANVNT--TSAP-----PVQTDIVNTSSISDLENQVLMQEKALS 410
Db 509 FKTRQGMQAKQPCAGTIGVSTYLCLAPDGIWDPOGPDLSNCS--SPWVNHITQKLKS-- 564
QY 411 LGSLEPNLAGEMINQVSKLLNS-----PDMLAPL----- 440
Db 565 -GETAANIARELAEQTRNHLNAGDITYSVRAMDQLVGLDVLQRLNLTGPGKDSAARSLNK 623
QY 441 -----AQLLKVVDDIGLQNLNSN-----TTISLTPSPSLALAVIR---VNAS 479
Db 624 LQKRESCRAVQAVQAVETVNNL-LQPQALNAWRDLTTSQDLRAATMLLDTVESAFVLAD 682
QY 480 SNTNSTTLLVN--NDCSVHAS--GNGNASTERNRGVSFVQNGD 995
Db 683 NLLKTDIVRENTDNIQLEVARLSTEGNLEDKPEPTGHTGHTSTIOLSAANTLKQNGRNGEIR 742
QY 531 VQNFET--PALFQDPSPLENLSL-----ISVVISSVANLTVRN-----LTVNVT 571
Db 743 VAFVLYNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAAINKFESKVKYVLAD 798
QY 572 NVTVTLKHINPSQDELTVRCVFDLGRNGRGWSDNGSCSVKDRRLNETICTCSHLTSG 631
Db 799 PVVTVKHIKQSEENFNCSEFWSYKRTWTGWSGTQGRLLTNTKTHHTTCSNHLTNFA 858
QY 632 VLL---DLRSTSVLPQAMALFTIYIGGLSSIFSLVTLVITYIAFEKIRDYPSKILLI 688
Db 859 VLMARVVKHSDAV--HDLDDVITWVIGILLSVCLLCITFTCFRGLQSD-RNTIHKN 915
QY 689 LCAALLNLVFL-----DSWIALYKMGGLCISVAVFLHYFLVSVTWMLGFAFMYLA 743
Db 916 LCISLFAELLFLIGINRTOPTA-----CAVFAALLHFFFLAAFTWMLFEGVQLYIM 968
QY 744 LVKVENT--YIRKYILKFCIVGVAVVTVITLTISPDNVLGSGYKFPNGSPDDFCW 801
Db 969 LVEVFESHSRRKY---FVLVGYGMPALIVAVSAVDYRSYG-----TDKVCW 1014
QY 802 NNAVFTVTVGVFCVIFLLNVSMFIVLVQLCRIKK--KKOLGAQRKTSIODLRSIAGL 859
Db 1015 RLDTYFIWFSFIGPATLIIMLVIFLGLYALYKMFHTTALPKESGLDNKISWVIGAI-L 1073
QY 860 TFLGITWGAFFAFGPNVNTFMFLAINTLQGGFIIFYCVAKENVRKQWRRL---C 916
Db 1074 LCLLGLTWAGLWYNINVESTIMAYLFTIENSLOGMFIPIHCVLQKVKYKGLRTHC 1133
QY 917 C-----GKRLAENSWSKATNGLKKQTVNGVSSSSNSLQSS 956
Db 1134 CSGRSTESSIGSGKTSGRTPGYSQSRIRRMWNTVRKOSSEFITGDINSSASLN 1193
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QY 957 NSTNSTLLVNDCSVHASGN 977
DB 1194 RGAMANHLISNALLRPHGTNN 1214
RESULT 16
O97826 PRELIMINARY; PRT; 1342 AA.
AC O97826;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LATROPHILIN 3 SPLICE VARIANT BBAH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148828; PubMed=10025961;
RA Matsushita H., Lelianova V.G., Ushkaryov Y.A.;
RT "The latrophilin family: multiply spliced G protein-coupled receptors
with differential tissue distribution.";
RL FEBS Lett. 443:348-352(1999).
DR EMBL; AF111093; AAD05329.1; .
DR InterPro; IPR000922; Gal_lectin.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR003334; Latrophilin.
DR InterPro; IPR003112; Olfac_like.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02140; Gal_Lectin; 1.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR Pfam; PF02354; Latrophilin; 1.
DR Pfam; PF02191; OLF; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRODOM; PD005612; Gal_lectin; 1.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; Hormr; 1.
DR SMART; SM00284; OLF; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS00228; SUEL_LECTIN; 1.
SQ SEQUENCE 1342 AA; 149658 MW; 51FBC79F37FF5B4B CRC64;
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Query Match 10.0%; Score 534; DB 6; Length 1342;  
Best Local Similarity 23.94; Pred. No. 8.5e-29;  
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;

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QY 260 LODPIVCLADHPRGPPFSSOSIPVVRATVLSQVFKATSFAPPDYSPVTHNVPSPIGE 319
DB 477 ISPIHLDSLRLPVRISTGPGTSTTTLRTT-----WSPGRSTTPSVGR 530
QY 320 IQLSPOPSAPIASSPAIDMPQSETISSPMPQTHVSGTPPPVKAFSS----- 368
DB 531 RNRSTSTP-----SPAELVNDI-----THVPSASQIPALAESCEAVEAREIMW 576
QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLENQVQLQMEKALS 410
DB 577 FKTRQGMQKQPCAGTIGTYLCLAPDGIWDGPDLSNCS--SPWNHITQKLKS-- 632
QY 411 LGSLEPNLAGEIMINQVSRLLHS-----PPDMLAPL----- 440
DB 633 -GETAANIARELAQTRNHLNAGDITYSVRANDQLVGLDVLQRLNTPGKDSAAARSLNK 691
QY 441 -----AORLLKVDDIGIQLNFSN-----TTISLTSPSLALAVIR----VNAS 479
DB 692 LQRRERSCRAYVOAMVETVNNL-LQOQALNAWRDLTTSQDLRAATMLDITVEESAFVLAD 750
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QY 480 SPNTTTFVAQDPANLQVLSLETOAPENSIGTITLPSL-----MNNLPAMDMLASR 530
DB 751 NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPEPNTGHGSTIQLSANTLQKNGRGEIR 810
QY 531 VQNFET--PALFQDPSLENLSL-----ISYVISSSVANLTVERN-----LFR 571
DB 811 VAFVLYNNLGPYL----STENASMKLGTAMSTNHSIVNPSVITAAINKERSNKVYLAD 866
QY 572 NVTYTLKHINPSQDELTVRCVFDLGRNGRGSGVSDGSCVKDRRLNETICTCSHLTSFG 631
DB 867 PVVFTVKHIKQSEENPNPCSEWSYKRTWTGYWSTQCRLLTTNKTHTCTSCNHLTNEA 926
QY 632 VLL----DLSTRTSVLPQAMMALFTITYIGCGLSLSTFLSVTLVITYIAFEKIRRDYPSKILIQ 688
DB 927 VLMHVEVKHSDAV--HDLDDVITWVGILLSLVCLLCIFTCFCFGLQSD--RNTIHK 983
QY 689 LCAALLLNLVFL-----DSWIALYKMOGLCISAVFLHYFLVLSFTWMGLEAFHMYLA 743
DB 984 LCISLFAELLFLIGINRTDPIA-----CAVFAALLHEFFLAFTWMFLEGVQLYIM 1036
QY 744 LVKVNT--YIRKYILKFCIVGWGPAVVVTIILITISPDNYGLSGYKPPNGSPDDFCWI 801
DB 1037 LVEVFESEHSRRKY---FYLVGYPALIVAVSAADVRSYG-----TDKVCWL 1082
QY 802 NNAVFYITVVGCFVIFLLNVSMFIVVLVOLCHRIK--KKQLGAQRKTSIQDLRSIAGL 859
DB 1083 RLDYFIWFSFGPATLIILNVLFLGIALYKMFHTAILKPESGCLDNKSVVIGAI-A-L 1141
QY 860 TFLGITWGFAPFAMGPVNVTFMYLFAINFLOQFFIFCYCAKENVRKOWRRYL---C 916
DB 1142 LCLLGLTWAFGLMYINESIVIMAYLFTFNSLQGMFIFHCVLQKVKYKGLRTHC 1201
QY 917 C-----GKRLAENSMDSKTATNGLKKQTVNQCQVSSSSLSQSS 956
DB 1202 CSGRSTESSIGSKTSGSRTPGRYSTGSGSRIRRMWMDTVRKQSESSITGDNSSASLN 1261
QY 957 NSTNSTLLVNDCSVHASGN 977
DB 1262 RGAMANHLISNALLRPHGTNN 1282
RESULT 17
O97811 PRELIMINARY; PRT; 1450 AA.
AC O97811;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE LATROPHILIN 2 SPLICE VARIANT BBAF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148828; PubMed=10025961;
RA Matsushita H., Lelianova V.G., Ushkaryov Y.A.;
RT "The latrophilin family: multiply spliced G protein-coupled receptors
with differential tissue distribution.";
RL FEBS Lett. 443:348-352(1999).
DR EMBL; AF111078; AAD05314.1; .
DR InterPro; IPR000922; Gal_lectin.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR003334; Latrophilin.
DR InterPro; IPR003112; Olfac_like.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02140; Gal_Lectin; 1.
DR Pfam; PF01825; GPS; 1.
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Db 409 ISPIHLDSDLRPPVREISTGTGPGTSTTTTLRTTT-----WSPGRSTTPSVSGR 462  
QY 320 IQPLSPQSPAPIASSPAIDMPPQSETISSPMPQTHVSGTTPPVKASFSS----- 368  
Db 463 RNRSTSTP-----SPAIEVLNDI-----THVPSASQIPALESCAEVAREIMW 508  
QY 369 -----PTVSAPANVNT--TSAP-----PVQTDIVNTSSIDLENQVLMKALS 410  
Db 509 FKTRGOMAKQPCPAGTIGVSTVLCCLAPDGIWDQPGDLSNCS--SPVNVHITQKLKS-- 564  
QY 411 LGSLEPNLAGEINQVSRLLHS-----PPDMLAPL----- 440  
Db 565 -GETAANIARELAEOITRNHILNAGDITYSVRAMDQVLGLLDVQLRNLTPGKDSAARSLNK 623  
QY 441 -----AORLLKVVDDIGLQNFN-----TTISLTSPSLALAVIR-----VNAS 479  
Db 624 LQKRSCRAYVOAMVETVNNL--LQPALNAWRDLTSDQLRAATMLDITVEESAFVLAD 682  
QY 480 SNFTTTFVAQDPANLOVSLETQAPENSIGTITLPSLL-----MNNLPAHDMELASR 530  
Db 683 NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLQONGRNGEIR 742  
QY 531 VQNFET--PALFQDPSLENLSL-----ISVIVSSVANLTVRN-----LTR 571  
Db 743 VAFVLYNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAAINKFESNKVYLAD 798  
QY 572 NVTVTLKHINPQDELTVRCVFDLGRNGRGWSDNGSCSVKDRRLNETICTCSHLTSPG 631  
Db 799 PVFTVKHIKQSEENFNPCSWFSYKRTWTGYWSTQGCRLTTNKHTTCSNHLTNFA 858  
QY 632 VLL---DLSRTSVLPQAMMALFTITVIGCGLSIFLSVTLVITYIAFEKIRRDYPSKILIQ 688  
Db 859 VLMAHVEVKHSDAV--HDLDDVITWVGILLSLVCLLICITFCFCFRGLQSD--RNTIHN 915  
QY 689 LCAALLNLNLVFL-----DSWIALYKMQGLCISVAVFLHVLVFTWGLFAHMYLA 743  
Db 916 LCISLFAELLFLIGINRTDQPIA-----CAVFAALLHFFFLAAFTWMLFEGVQLYIM 968  
QY 744 LVKVENT--YIRKYLKFCIVGMPVAVVITIIITISPDNKGGLSGYKGFPGSPDFCWI 801  
Db 969 LVEPSEHSRRKY---FVLGVGMPALIVAVSAADVRSYG-----TPKVCWL 1014  
QY 802 NNAVYITVGVFCVIFLLNYSFMFIVLVOLCRICK--KQLGAQRKTSIQDLRSIAGL 859  
Db 1015 RLDTYIFSWFICPATLIIMLVIFGLIYALYKMFHHTAILKPESGCLDNKSWVIGAI--L 1073  
QY 860 TELGITWGFAPFAGPVNVTFEYLFPAINTLOGFFTFIFCYVAKENVRKOWRRYL--C 916  
Db 1074 LCLGLTWFAGFLMYNESIVIMAYLFTIENSLQGMFIFHCVLQKKVRKEYGKLRTHC 1133  
QY 917 C-----GKRLRAENSWSKATNGLKKTQVNOGVSSSSNSLQSSS 956  
Db 1134 CSGRSTESSIGSKTSGSRTPGRYSTGSGSRIRRMWMDTVRKQSESSFITGDINSSASIN 1193  
QY 957 NSTSTLLVNDCSVHASN 977  
Db 1194 RGAMANHLISNALLRPHGNTN 1214

RESULT 19  
O97824 PRELIMINARY; PRT: 1571 AA.  
AC O97824;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE LATROPHILIN 3 SPLICE VARIANT BBAF..  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC NCBI\_TaxID=9913;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=99148928; PubMed=10025961;  
RA Matsushita H.; Lelianova V.G.; Ushkaryov Y.A.;  
RT "The latrophilin family: multiply spliced G protein-coupled receptors  
RL with differential tissue distribution.";  
FEBS Lett. 443:348-352(1999).  
DR EMBL; AF111091; AAD05327.1; .  
DR InterPro; IPR000922; Gal\_lectin.  
DR InterPro; IPR000832; GPCR\_secretin.  
DR InterPro; IPR001879; horrmn\_receptor.  
DR InterPro; IPR003334; Latrophilin.  
DR InterPro; IPR003112; Olfac\_like.  
DR InterPro; IPR000203; PKD\_cys\_rich.  
DR Pfam; PF00002; 7tm\_2; 1.  
DR Pfam; PF02140; Gal\_lectin; 1.  
DR Pfam; PF01825; GPS; 1.  
DR Pfam; PF02793; HRM; 1.  
DR Pfam; PF02354; Latrophilin; 1.  
DR Pfam; PF02191; OLF; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PRODOM; PD005612; Gal\_lectin; 1.  
DR SMART; SM00303; GPS; 1.  
DR SMART; SM00008; Hormr; 1.  
DR SMART; SM00284; OLF; 1.  
DR PROSITE; PS50227; G\_PROTEIN\_RECP\_F2\_3; 1.  
DR PROSITE; PS50261; G\_PROTEIN\_RECP\_F2\_4; 1.  
DR PROSITE; PS50228; SUEL\_LECTIN; 1.  
SQ SEQUENCE 1571 AA; 174901 MW; 2185D5ADCB5F8607 CRC64;

Query Match 10.0%; Score 534; DB 6; Length 1571;  
Best Local Similarity 23.9%; Pred. No. 1e-28;  
Matches 206; Conservative 124; Mismatches 333; Indels 198; Gaps 30;

QY 260 LODPIVCLADHPRGPPFSSQSIPVVRATVLSQVPKATSPAEPPDYSPVTHNVPSPIGE 319  
Db 477 ISPIHLDSDLRPPVREISTGTGPGTSTTTTLRTTT-----WSPGRSTTPSVSGR 530  
QY 320 IQPLSPQSPAPIASSPAIDMPPQSETISSPMPQTHVSGTTPPVKASFSS----- 368  
Db 531 RNRSTSTP-----SPAIEVLNDI-----THVPSASQIPALESCAEVAREIMW 576  
QY 369 -----PTVSAPANVNT--TSAP-----PVQTDIVNTSSIDLENQVLMKALS 410  
Db 577 FKTRGOMAKQPCPAGTIGVSTVLCCLAPDGIWDQPGDLSNCS--SPVNVHITQKLKS-- 632  
QY 411 LGSLEPNLAGEINQVSRLLHS-----PPDMLAPL----- 440  
Db 633 -GETAANIARELAEOITRNHILNAGDITYSVRAMDQVLGLLDVQLRNLTPGKDSAARSLNK 691  
QY 441 -----AORLLKVVDDIGLQNFN-----TTISLTSPSLALAVIR-----VNAS 479  
Db 692 LQKRSCRAYVOAMVETVNNL--LQPALNAWRDLTSDQLRAATMLDITVEESAFVLAD 750  
QY 480 SNFTTTFVAQDPANLOVSLETQAPENSIGTITLPSLL-----MNNLPAHDMELASR 530  
Db 751 NLLKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLQONGRNGEIR 810  
QY 531 VQNFET--PALFQDPSLENLSL-----ISVIVSSVANLTVRN-----LTR 571  
Db 811 VAFVLYNNLGPYL-----STENASMKLGTEAMSTNHSVIVNSPVITAAINKFESNKVYLAD 866  
QY 572 NVTVTLKHINPQDELTVRCVFDLGRNGRGWSDNGSCSVKDRRLNETICTCSHLTSPG 631  
Db 867 PVFTVKHIKQSEENFNPCSWFSYKRTWTGYWSTQGCRLTTNKHTTCSNHLTNFA 926  
QY 632 VLL---DLSRTSVLPQAMMALFTITVIGCGLSIFLSVTLVITYIAFEKIRRDYPSKILIQ 688  
Db 927 VLMAHVEVKHSDAV--HDLDDVITWVGILLSLVCLLICITFCFCFRGLQSD--RNTIHN 983  
QY 689 LCAALLNLNLVFL-----DSWIALYKMQGLCISVAVFLHVLVFTWGLFAHMYLA 743  
Db 984 LCISLFAELLFLIGINRTDQPIA-----CAVFAALLHFFFLAAFTWMLFEGVQLYIM 1036

QY 744 LKVFNT--YIRKYLKFCIVGCVPAVVVITLITSPDNVGLSGYGFPPNGSPDDFCWI 801  
 DB 1037 LVEFSEHSRRKY---FYLVGMPALIVAVSAADYRSYG-----TDKVCWL 1082  
 QY 802 NNNAVFTVVGVCVIFLLNVSMFIVVLVOLCRICK--KKQLGAQRKTSIODLRSIAGL 859  
 DB 1083 RDTYFVWSFGPATLIIMLVIFGLTALYKMFHHTAILKPESGCLDNKISVWVIGAI-L 1141  
 QY 860 TFLGLTGWFAFFAWGPNVNTFMYLFAIFNTLQGFFFIFCYCAKENVRKQWRRYL---C 916  
 DB 1142 LCLGLTWARFCLMVTINVESTIMAYLFTIFNSLQGMFIFIFHCVLQKVKRYGKCLRTHC 1201  
 QY 917 C-----GKRLAENSQWSTATNGLKQKQTVNOGVSSSSNSLSQSS 956  
 DB 1202 CSGRSTESSGSGKTSRTPGCRYSTGQSRIRRMWMDTVRKQSESSFITGDNSSASLN 1261  
 QY 957 NSTNSTLLVNDSCSVHASGN 977  
 DB 1262 RGAMNHLISNALLRPHGTNN 1282  
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 ID O97822 PRELIMINARY; PRT: 1240 AA.  
 AC O97822;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE LATROPHILIN 3 SPLICE VARIANT ABGG.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99148828; PubMed=10025961;  
 RA Matsushita H., Lellanova V.G., Ushkaryov Y.A.;  
 RT "The latrophilin family: multiply spliced G protein-coupled receptors  
 RT with differential tissue distribution."  
 RL FEBS Lett. 443:348-352(1999).  
 DR EMBL; AF11089; AAD05325.1; -.  
 DR InterPro; IPR000922; Gal\_Lectin.  
 DR InterPro; IPR000832; GPCR\_secretin.  
 DR InterPro; IPR001879; hormn\_receptor.  
 DR InterPro; IPR003334; Latrophilin.  
 DR InterPro; IPR003112; Olfac\_Like.  
 DR InterPro; IPR000203; PKD\_cys-rich.  
 DR Pfam; PF00002; 7tm2; 1.  
 DR Pfam; PF02140; Gal\_Lectin; 1.  
 DR Pfam; PF01825; GPS; 1.  
 DR Pfam; PF02793; HRM; 1.  
 DR Pfam; PF02354; Latrophilin; 1.  
 DR Pfam; PF02191; OLF; 1.  
 DR PRINTS; PR00249; GPCRSECRETIN.  
 DR PRODOM; PD005612; Gal\_Lectin; 1.  
 DR SMART; SM00303; GPS; 1.  
 DR SMART; SM00008; Hormn; 1.  
 DR SMART; SM00284; OLF; 1.  
 DR PROSITE; PS00227; G-PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE; PS00261; G-PROTEIN\_RECEP\_F2\_4; 1.  
 DR PROSITE; PS00228; SUEL\_Lectin; 1.  
 SQ SEQUENCE 1240 AA; 139349 MW; 23E8B26D48F88131 CRC64;

Query Match 10.0%; Score 533.5; DB 6; Length 1240;  
 Best Local Similarity 24.2%; Pred. No. 8.2e-29;  
 Matches 209; Conservative 123; Mismatches 345; Indels 187; Gaps 31;  
 QY 260 LQDPTVCLDHPGRPPFSSSQSIPVPRATVLSQVFKATSFABPPDYSPVTHNVPSPIGE 319  
 DB 409 ISPPHLDSDLRPPVRESITGGLGTSTTTTLRTIT-----WSPGRSTTPSVSGR 462

QY 320 IQPLSPOPSAPIASSPAIDMPQSETISSPMQTHVSGTPPPVKKASFSS----- 368  
 DB 463 RNRSTSP-----SPAELVNDI-----TTHVPSASPOIPALEESCEAVEAREIMW 508  
 QY 369 -----PTVSAPANVT--TSAP-----PVQTDIVNTSSISDLNOVLQMEKALS 410  
 DB 509 FKTRQGMOKQPCPAGTIGVSTYLCLAPDGIWDPOGPDLSNCS--SPWVNHITQKLKS-- 564  
 QY 411 LGSLEPNLAGEMINQVSRLLHS-----PPDMLAPL----- 440  
 DB 565 -GETAANIARELAETRNLNAGDITYSVRAMDQLVGLLDVQLRNLTPGCKDSAAASLNK 623  
 QY 441 -----AQRLLKYVDDIGLQNFNSN-----TTISLTSPSLALAVIR--VNAS 479  
 DB 624 LQKRESCRAYVQAMVETVNNL-LQPAALNAWRDLTTSQDRAATMLLDTVEESAFVLAD 682  
 QY 480 SFNTTTFVAQDPANLQVLETOAPENSIGTITLPPSL-----MNNLPAMDLMELASR 530  
 DB 683 NLLKTDIVRENTDNIQLEVARLSTEGNEDLKPENTGHSTIQLSANTLQNGRNGEIR 742  
 QY 531 VOENFFET--PALFODPSLENLSL-----ISYVISSSVANLTVRN-----LTR 571  
 DB 743 VAFVLYNNLGPYL---STENASMKLGTTEAMSTNHSVIIVNSPVITAAINKEFSNKVYLAD 798  
 QY 572 NVTVLKHINPSQDELTVRCVFWDLGRNGRGWSDNGSVKDRRLNETTCTCSHLTSFG 631  
 DB 799 PVFTVVKHIKQSEENFNPCSPWSYSKRTMTGYWSTQGCRLLTNTKTHTTCSNHLTNFA 858  
 QY 632 VLL---DLSTRSVLPAQMMALTFIYIGGLSIFLSVTLVTVIAPEKIRRDYPSKILIQ 688  
 DB 859 VLMHVEVKHSDAV--HDLLDVIITWGIILSLVCLLICIFTCFFRGLQSD-RNTIHN 915  
 QY 689 LCAALLLNLLVPLL-----DSWTALYKMOGLCISVAVFLHYFLVLSFTMGLEAFHMYLA 743  
 DB 916 LCISLFAELFLFIGNRTDQPIA-----CAVFAALLHFFELAAFTWFMLEGVQLYIM 968  
 QY 744 LKVFNT--YIRKYLKFCIVGCVPAVVVITLITSPDNVGLSGYGFPPNGSPDDFCWI 801  
 DB 969 LVEVPESEHSRRKY---FYLVGMPALIVAVSAADYRSYG-----TDKVCWL 1014  
 QY 802 NNNAVFTVVGVCVIFLLNVSMFIVVLVOLCRICK--KKQLGAQRKTSIQDLR----- 854  
 DB 1015 RLDYTFWISFGPATLIIMLVIFGLTALYKMFHHTAILKPESCLDNINVEDNRPFIKS 1074  
 QY 855 ---STAGTLFLGITWGFAGFPVNVTFMYLFAIFNTLQGFFFIFCYCAKENVRKQW 911  
 DB 1075 WVIGATALLCLGLTWARFCLMVTINVESTIMAYLFTIFNSLQGMFIFIFHCVLQKVKRY 1134  
 QY 912 RRYL---CCGKRLAENSQWSTATNGLKQKQTVNOGVSSSSNSLSQSSNSTNTLLVNN 968  
 DB 1135 GKCLRTHCCSG-RSTESSIGSGKTSRTPGCRYSTGQSRIRRMWMDTVRKQSESSFITG 1193  
 QY 969 DCSVHASGNAGNASTERN-GVSFSV 991  
 DB 1194 DINSSASLNREPYPRTSMGVKLNI 1217  
 PRELIMINARY; PRT: 1308 AA.  
 ID O97828  
 AC O97828;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE LATROPHILIN 3 SPLICE VARIANT BBBG.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.



QY	571	RNVTVLKHINPSQDELTVRCVFWDLGRNGRGWSDNGCSVKDRRLNETICTCSHLTSP	630
DR		PROSITE; PS50261; G_PROTEIN_RECEP_F2_3; 1.	
DR		PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.	
DR		PROSITE; PS00904; PPTA; UNKNOWN.1.	
DR	210	DPVFTVKHIGSEENFNPCSEFWSKRTMTGYSTQGRLLTNTKTHTTCSCHLNTNF	269
DR		PROSITE; PS50228; SUELLECTIN.1.	
DR		SEQUENCE 1407 AA; 157657 MW; 01AF1591513D2C48 CRC64;	
QY	631	GVLL---DLSRTSVLPQAMALFITVIGGLSIFLSVTLVTYIAFEKIRRDYPSKILI	687
DR		Query Match 9.9%; Score 531.5; DB 6; Length 1407;	
DR		Best Local Similarity 24.2%; Pred. No. 1.4e-28;	
DR		Matches 238; Conservative 161; Mismatches 422; Indels 225; Gaps 48;	
QY	688	QLCAALLLNLVFL---DSWTALYKMOGLCISVAVFLHYFLVSVFTWGLEAFHMYL	742
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	327	NLCISLFAVELLFLIGINRDTQPIA-----CAVFAALLHFFFLAATWMPLEGVQLYI	379
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	743	ALVKVNT---YIRKYILKFCIVGCVGPAVVVITILTISPNDYGLSGYKFPNGSPDDFCW	800
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	380	MLVEVFESEHSRRKY---FYLVGCMPLIIVAVSAADVRSYG-----TDKVCW	425
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	801	INNAVFIITVGVFCVFIELNVSMFIVLVQLCRKK--KKOLGAQRKTSIQDLRSIAG	858
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	426	LRDITFIWFGIPATLIILNLNVIFLGLYALKMFHTAILKPESCLDNIKSWVICAIA-	484
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	859	LTELLGITWGAFFAWGPNVNTFMFLFAINFNLQGFIFIFCYVAKENVKOW-----RRY	914
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	485	LLCLGLTFAWGLMYNESTVIMAYLFTIENSLOGMFIFIFHCVLQKKVKEYGKCLRTH	544
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	915	LCGKGL-----RLAENS-----WSKTATNGLKKOTVNOGVSSSSNS	951
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	545	CCSGSTESSIGSGKTSRPPGRYSTGSRIRKMNNDT-----VRKQSESFITGDIN-	599
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	952	LQSSNSTNTLLVN--NDCSVHAS--GNGNASTERNVGSFVSQNGD	995
DR		PROSITE; PS50228; SUELLECTIN.1.	
QY	600	---SSASLNREGLLNARDTSVMDTLPLNGN-----HGNSYSIASGE	638
DR		PROSITE; PS50228; SUELLECTIN.1.	
DR	RESULT	23	
DR	O97810	PRELIMINARY; PRT; 1407 AA.	
DR	AC	O97810	
DR	DT	01-MAY-1999 (Tremblrel. 10, Created)	
DR	DT	01-MAY-1999 (Tremblrel. 10, Last sequence update)	
DR	DT	01-OCT-2001 (Tremblrel. 18, Last annotation update)	
DR	DE	LATROPHILIN 2 SPLICE VARIANT BBAE.	
DR	OS	Bos taurus (Bovine).	
DR	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
DR	OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
DR	OC	Bovidae; Bovinae; Bos.	
DR	OX	NCBI_TaxID=9913;	
DR	RN	[1]	
DR	RP	SEQUENCE FROM N.A.	
DR	RX	MEDLINE=99148826; PubMed=10025961;	
DR	RA	Matsushita H., Lellanova V.G., Ushkaryov Y.A.;	
DR	RT	"The latrophilin family: multiply spliced G protein-coupled receptors	
DR	RT	with differential tissue distribution."	
DR	RL	FEBS Lett. 443:348-352(1999).	
DR	DR	EMBL; AF111077; AAD05313.1; -	
DR	DR	InterPro; IPR000922; Gal.lectin.	
DR	DR	InterPro; IPR000832; GPCR_secretin.	
DR	DR	InterPro; IPR001879; hormn_receptor.	
DR	DR	InterPro; IPR003334; Latrophilin.	
DR	DR	InterPro; IPR003112; Olfac. like.	
DR	DR	InterPro; IPR00203; PKD_cys_rich.	
DR	DR	InterPro; IPR002088; PPTA.	
DR	DR	Pfam; PF00002; 7tm2.2; 1.	
DR	DR	Pfam; PF02140; Gal.lectin; 1.	
DR	DR	Pfam; PF01825; GPs; 1.	
DR	DR	Pfam; PF02793; HRM; 1.	
DR	DR	Pfam; PF02354; Latrophilin; 1.	
DR	DR	Pfam; PF02191; OLF; 1.	
DR	DR	PRINTS; PR00249; GPCRSECRETIN.	
DR	DR	ProDom; PD005612; Gal.lectin; 1.	
DR	DR	SMART; SM00303; GPs; 1.	
DR	DR	SMART; SM00008; Hormn; 1.	
DR	DR	SMART; SM00284; OLF; 1.	

Db 1028 VLGAFAALLCLLGLTWSFGLLFINETIVMAYLFTIFNAFGVFIPIFHCALQKVRKEYG 1087  
 QY 912 ---RRYLCCKL-----RLAENSWSKATNGLKKQTVNOGVSSSNSLQ 953  
 Db 1088 KCFRHSYCGGLPTESPHSVKASTTFTSARYSGTOSRIERMWNTVRKQSESSFISGD 1147  
 QY 954 SSSNSTNTLLVNDCSVHAG-----NGNASTERNGVSFSVQNGD 995  
 Db 1148 INSTSTLNOGHSLLNARDTSAMDTLPLNGFNN-----SYSLRKG 1188

RESULT 24  
 Q92173 PRELIMINARY: PRT: 1550 AA.  
 ID Q92173  
 AC Q92173;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE CALCIUM-INDEPENDENT ALPHA-LATROTOXIN RECEPTOR HOMOLOG 3.  
 GN CIRL-3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99150330; PubMed=10026162;  
 RA Ichtchenko K., Bittner M.A., Krasnoperov V., Little A.R., Chepurny O.,  
 RA Holz R.W., Petrenko A.G.;  
 RT "A novel ubiquitously expressed alpha-latrotoxin receptor is a member  
 RT of the CIRL family of G-protein-coupled receptors.";  
 RL J. Biol. Chem. 274:5491-5498(1999).  
 DR EMBL; AF063103; AAC7816.1; .  
 DR InterPro; IPR000922; Gal.lectin.  
 DR InterPro; IPR000832; GPCRsecretin.  
 DR InterPro; IPR01879; hormn.receptor.  
 DR InterPro; IPR003334; Latrophilin.  
 DR InterPro; IPR003112; Olfac.lik.  
 DR InterPro; IPR000203; PKD\_cys\_rich.  
 DR Pfam; PF00002; 7tm2; 1.  
 DR Pfam; PF02140; Gal.Lectin; 1.  
 DR Pfam; PF01825; GPS; 1.  
 DR Pfam; PF02793; HRM; 1.  
 DR Pfam; PF02354; Latrophilin; 1.  
 DR Pfam; PF02191; OLF; 1.  
 DR PRINTS; PR00249; GPCRSECRETIN.  
 DR PRODOM; PD005612; Gal.lectin; 1.  
 DR SMART; SM00303; GPS; 1.  
 DR SMART; SM00008; Hormr; 1.  
 DR SMART; SM00284; OLF; 1.  
 DR PROSITE; PS50227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE; PS50261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 DR PROSITE; PS50228; SUEL\_LECTIN; 1.  
 KW Receptor.  
 SQ SEQUENCE 1550 AA; 172441 MW; A2E8091B2B34DB36 CRC64;

Query Match 9.9%; Score 531.5; DB 11; Length 1550;  
 Best Local Similarity 24.0%; Pred. No. 1.5e-28;  
 Matches 216; Conservative 135; Mismatches 347; Indels 203; Gaps 35;

QY 248 SSPELGLQCDLQDPIVCLADHPRGPPSSSSIPVPRATVLQVPRKATSFAPPPDYS 307  
 Db 466 SGPVHGVQSV-ISPPIHLSDLRPPVRGISTGLPGMGSTTTTLRTTWNLGRSTT 524  
 QY 308 PV-----THNVPSPIGEIQLPQSPAPIASSPAIDMPQSETISSPMPQTHVSGTTP 360  
 Db 525 PSLGRRNRSTPTSP--AIEVLDVTHLPSSAASIPAMBEESCEAVEAREIMWPKTRQG 582  
 QY 361 PVKASFSSPTVS-----APANVNTTAPPVOTDVNTSSISDLENQVLMERALSLS 413  
 Db 583 VAKOSCPAGTIGVSYLCLAPDGIWDPQGP---DLSNCS--SPWNHITQKLKS---GE 633

QY 414 LEPNLAGEMINVSRLLHS-----PPDMLAPL----- 440  
 Db 634 TAANIARELAETRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSARSLNKLOK 693  
 QY 441 -----AORLLKVVDDIGLQNFNS-----TTISLTPSLALAVIR-----VNASSFN 482  
 Db 694 RERSCRAYVQAMVETVNNL-LQPALNAWRDLTTSQDLRAATMLLDTVESAFVLADNLL 752  
 QY 483 TTFVQAQDPANLQVSLQAPENSIGTITLPPSL-----MNNLPAHDMELASRVQF 533  
 Db 753 KTDIVRENTDNIQLEVARLSTEGNLEDKFPENTGHSTIQLSANTLKONGRNGEIRVAF 812  
 QY 534 NEFET--PALFQDPSLENLSL-----ISYVSSVANLTVRN-----LTRNVT 574  
 Db 813 VLYNNGPVL-----STENASMKLGTEAMSTNHSIVNSPVITAAINKEFSNKVILADPV 868  
 QY 575 VTLKIINQSODELTVRVCVFDLGRNGRGWSDGSCVKDRRLNETICTCSHLTSPGVLL 634  
 Db 869 FTVKHIKQSEENFPNCSFWSYSKRTMTGYNSTQGCRLTTNKTHTTSCNHLTNFAVILM 928  
 QY 635 ---DLRSRTSVLPAQMMALFTITVIGCGLSISIFLSTVLTVTYIAFEKIRRDYPSKILLQLCA 691  
 Db 929 AHVEVKHSDAV--HDLLLDVITWVGILLVCLLICITFTCFEFGQSD--RNTIHKNLCI 995  
 QY 692 ALLLLNLVFL-----DSWIALYKMOGLCISAVFLHYFLVSVFTWGLGFAFMYLALVK 746  
 Db 986 SLFVAELLFLIGINRDTQPIA-----CAVFAALLHFFELAAFTWFLGVLQYIMLVE 1038  
 QY 747 VENT--YIRKYILKFCIVGWGPVAVVTIILTISPDNVGLSGYKFPNGSPDDFCWINN 804  
 Db 1039 VFSEHSRRKY---FYLVGYGMPALIVAVSAADVRSYG-----TDKVCWLRLD 1084  
 QY 805 AVFYTVVGYFCVIFLLNVSMFTVLVQLCRICK--KKOLGAQRKTSIODLR----- 854  
 Db 1085 TYFHSFGPATLIIMLVIFGLIALYKMFHHTAILPESCLONINEDNRPFTKSWYI 1144  
 QY 855 SIAGTLFLGITWGEFAFFAWGPVNVTFMYLFAINTLQGFIFIFYCYAKENVRKQW--- 911  
 Db 1145 GAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHCVLQKKVRKEYGKC 1204  
 QY 912 -RRYLCCGKL-----RLAENS-----WSKTATNGLKKQTVNOGVSS 947  
 Db 1205 LRTHCCSGKSTESSGSGKTSRTPGRTGSGSRIRRMNDT----VRKOSESFTIG 1260  
 QY 948 SSNSLQSSNSTNTTL-----LVNN--DCSVHAS--GNGNASTERNGVSFSVQNG 994  
 Db 1261 DINSSASLNRGSLYLCIQACVTVYLEGLLNARDTSVMDTLPNGN-----HGNSYSIAGG 1315  
 QY 995 D 995  
 Db 1316 E 1316

RESULT 25  
 O97819 PRELIMINARY: PRT: 1231 AA.  
 ID O97819  
 AC O97819;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE LATROPHILIN 3 SPLICE VARIANT ABAG.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99148828; PubMed=10025961;  
 RA Matsushita H., Lelianova V.G., Uskaryov Y.A.;  
 RT "The latrophilin family: multiply spliced G protein-coupled receptors  
 RT with differential tissue distribution.";  
 RL FEBS Lett. 443:348-352(1999).

